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RESULT 5

OBKFB5_CHITE

OBKFB5_CHITE PRELIMINARY; PRT; 361 AA.

AC QBKFB5_CHITE PRELIMINARY; PRT; 361 AA.

AC QBKFB5_CHITE PRELIMINARY; PRT; 361 AA.

AC QBKFB5_CHITE

Ol-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence;

Chlorobian pudate)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence of Chlorobiaceae;

Chlorobian update)

CC Chlorobian pudate)

DC ITEMBLREL 25, Last annotation update)

DC ITEMBLREL 25, Last annotation update)

DC ITEMBLREL 25, Last annotation update)

DC ITEMBLREL 25, Last sequence of Chlorobian update)

DT 01-OCT-2002 (TrEMBLREL 25, Last sequence of Chlorobian tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).

TO 10-OCT-2002 (TrEMBLREL 22, Created)

DT 01-OCT-2002 (TrEMBLREL 22, Last sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
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-1- SIMILARITY: Belongs to the ABC transporter family. EMBL; AE009247; AAL43996.1; -; Genomic DNA.

REMBL; AE009247; AAL43996.1; -; Genomic DNA.

EMBL; AE009247; AAL43996.1; -; Genomic DNA.

REMBL; AE009347; AAL43996.1; -; Genomic DNA.

REMBL; AE00935; D98335.

RGO; GO:0016887; F:ATP binding; IEA.

GO; GO:0016887; F:ATP binding; IEA.

GO; GO:0016887; F:ATPase activity; IEA.

RGO; GO:0016887; F:ATPase activity; IEA.

RO; GO:0016
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Goodner B., Hinkle G.
Qurollo B., Gold-
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3., Miller N., Blanchard M.,

, Askenazi M., Halling C., Mullin

, Iartchouk O., Epp A., Liu F.,

D., Scott C., Lappas C., Markelz B

J., Lomo C., Sear C., Strub G.,
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RA Rey M.W., Ra RA Tang M., Lop RA Clsen P.B., RA Fang M., Lop RA Clsen P.B., RA Ehrlich S.D.
RA Tang M., Lop RA Clsen P.B., RA Ehrlich S.D.
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                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.

R PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;

R PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;

R Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.

R Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.

R Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,

A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,

A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,

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A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,

A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,

A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,

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B Complete genome sequence of the industrial bacterium Bacillus specie icheniformis and comparisons with closely related Bacillus specie genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).

R EMBL; AE017333; AAU42873.1; -; Genomic_DNA.

R EMBL; CP000002; AAU25501.1; -; Genomic_DNA.

R GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf...

R GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf...

R InterPro; IPR0002478; PUA.

InterPro; IPR000051; SAM_bd.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0000166; F:nucleotide binding; I
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transp_like.
Pfam; PF00005; ABC_tran; 1.
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SMART; SM003
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PubMed=15383718; DOI=10.1159/000079829;

Veith B., Herzberg C., Steckel S., Feesche J.,

Ehrenreich P., Baeumer S., Henne A., Liesegang

Ehrenreich A., Gottschalk G.;
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J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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396 AA;
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49.5%; milarity 47.1%; Conservative
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(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 31, Last sequence update)
(And some other nucleotide) binding motif, PUA domain).
OrderedLocusNames=BL03857, BLi04060;
Cheniformis (strain DSM 13 / ATCC 14580).
Pirmicutes; Bacillales; Bacillaceae; Bacillus.
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larity 55.0%;
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1006; ABC_transporter; 1.
32; AAA; 1.
1893; ABC_TRANSPORTER_2; 1.
Complete_proteome; Membrane; Nucleotide-binding;
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; F:ATP binding; IEA.
; F:ATPase activity; IEA.
; F:hydrolase activity; IEA.
; F:nucleotide binding; IEA.
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n_I.G.,
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Q4HUZ1_GIBZE
Q4HUZ1;
ID Q4HUZ1;
AC Q4HUZ1;
DT 13-SEP-2005 (TrEMBLrel. 31, C)
DT 13-SEP-2005 (TrEMBLrel. 31, L)
DT 13-SEP-2005 (TrEMBLrel. 31, L)
DT 13-SEP-2005 (TrEMBLrel. 31, L)
DE Hypothetical protein.
GN ORFNames=FG11217.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota;
OC Hypocreomycetidae; Hypocreale
OX NCBI_TaxID=229533;
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Best Local
Matches 1
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EMBL; AF043702; AAK21492.3; -; Genembl; W03D8.6; Caenorhabditis e wormBase; WBGene00002174; itx-1.

WormPep; W03D8.6; CE32737.

InterPro; IPR006209; EGF 2.

InterPro; IPR006210; IEGF.

InterPro; IPR006210; IEGF.

InterPro; IPR012680; Laminin G.

Pfam; PF00008; EGF; 2.

SMART; SM00181; EGF; 2.

SMART; SM00282; Lamin G 2; 2.

SMART; PS000282; EGF 1; UNKNOWN 1

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS0026; EGF 3; 3.

PROSITE; PS0026; EGF 3; 3.
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01-JUN-1998 (TrEMBLrel. 06, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence upda

01-MAR-2004 (TrEMBLrel. 26, Last annotation up

Intestinal neurexin-like protein 1.

Name=itx-1; ORFNames=W03D8.6;

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rha
Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxID=6239;
 NUCLEOTIDE
STRAIN=PH-1
Birren B.,
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extant gymnosperms are monophyletic and Gnetales' Closest relacives T are conifers.";

I proc. Natl. Acad. Sci. U.S.A. 97:4092-4097(2000).

C -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

R EMBL; AF209109; AAF64667.1; -; Genomic_DNA.

R HSSP; P19483; 1H8E.

R GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0045261; C:proton-transporting ATP synthase complex, C....

GO; GO:0045261; C:proton-transporting two-sector ATPase complex; I.

GO; GO:0016469; C:proton-transporting ATP synthase activity....

GO; GO:0046933; F:hydrogen-transporting ATPase activity, rota....

GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota....

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid....
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A Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
A Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
A Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
A Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
A Hagopian D., Hagos B., Hall J., Horton L., Kamat A., Karatas A.,
A Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
A Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
A Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
A Nielsen C.B., Norbu C., O'Connor T., Naylor J., Nguyen C., Nicol R.,
A Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
A Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
A Rachupka A., Ramassamy U., Raymond C., Retta R., Rise C., Rogov P.,
A Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
A Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
A Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
A Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
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EMBL; AACM01000460; EA
Hypothetical protein.
SEQUENCE 368 AA; 40
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Name=atpA;
Gnetum ula.
Mitochondrion.
Eukaryota; Viridi
Spermatophyta; Gn
NCBI_TaxID=3383;
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01-OCT-2003
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Lander E.;

"Fusarium graminearum genome sequence.";

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
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                                                                                                                                                                                                                                                                                                                                                                                                                              26063; PubMed=10760278; DOI=10.1073/pnas.97.8.4092; Coat G., dePamphilis C.W.; of seed plants based on all three genomic compartments: losperms are monophyletic and Gnetales' closest relatives
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a; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum
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15, Last seq
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GO; GO:0006811; P:ion transport; IEA.

R GO; GO:0015992; P:proton transport; IEA.

R InterPro; IPR005294; ATP_synthF1_alph.

R InterPro; IPR004100; ATPase_a/b\[ N.

InterPro; IPR000194; ATPase_a/b\[ Centre.

R Pfam; PF00006; ATP-synt_ab; 1.

R Pfam; PF02874; ATP-synt_ab; 1.

R Pfam; PF02874; ATP-synt_ab; 1.

R PfGRFAMs; TIGR00962; atpA; 1.

R PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.

R PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.

NON_TER ATP-binding; CF(1); Hydrogen ion transport; Hydrogen transport;
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NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SUBJECT.

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Yta; Gnetophyta;
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(TrEMBLrel. 13, Last
(TrEMBLrel. 25, Last
a subunit (Fragment).
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Gnetopsida;
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4; Mismatc
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ransport; IEA.
                                                   transport;
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                        Transport
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RESULT 11
Q691P6 ORYSA
AC Q691P6;
DT 25-OCT-2004
DT 25-OCT-2004
DT 25-OCT-2004
DT 25-OCT-2004
DT 25-OCT-2004
OC Spermatophyta
OC Spermatophyta
OC Shrhartoideae
OX NCBI_TaxID=39
RN [1]
RN [1]
RN [1]
RA Sasaki T., Ma
RT "Oryza sativa
RT "Oryza sativa
RT clone:OSJNBa0
RT clone:OSJNBa0
RT clone:OSJNBa0
RT Go; GO:00041;
DR GO; GO:00065
DR InterPro; IPI
DR InterPro; IPI
DR Ffam; PF0002;
DR PFam; PR0002;
DR PRINTS; PR000050
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   RESULT
Q6BIS4
ID Q6BIS4
AC Q6
DT 25
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CO S1
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Matches
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Best Local
Matches
                                                                                                                                  QGBIS4 DEBHA PRELIMINARY; PRT; 1048 AA.

C QGBIS4;
C QGBIS4;
T 25-OCT-2004 (TrEMBLrel. 28, Created)
T 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
E Similar to CA1657 | IPF16022 Candida albicans IPF16022 unknown
E function.
E function.
C OrderedLocusNames=DEHA0G08679g;
S Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
C Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
C Saccharomycetales; Saccharomycetaceae; Debaryomyces.
X NCBI_TaxID=4959;
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NON_TER
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STRAIN=ATCC
PubMed=15229
      Dujon B., S
Lafontaine
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Local (
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1 (MAR-2004) to +1
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E SEQUENCE [LARGE SCALE GENOMIC DNA].
CC 36239 / CBS 767;
C2 36239 / CBS 767;
229592; DOI=10.1038/nature02579;
Sherman D., Fischer G., Durrens P., Casaregola
s I., de Montigny J., Marck C., Neuveglise C., T
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00792; PEPSIN.
S00141; ASP_PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194;
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508; P:proteolysis and peptidolysis;
PR001461; Peptidase_A1.
PR001969; Pept_Asp_AS.
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91P6; -.
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(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
partic proteinase nepenthesin I.
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Viridiplantae; Streptophyta; En
ta; Magnoliophyta; Liliopsida;
ae; Oryzeae; Oryza.
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Pred. No. 55;
4; Mismatches
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RESULT 13
Q8G456_BIFLO
ID Q8G456_BIFLO
AC Q8G456;
DT 01-MAR-2003
DT 01-MAR-2003
DT 01-MAR-2004
DE Fas.
GN Name=fas; Ordon
OS Bifidobacter:
OC Bifidobacter:
OX NCBI_TaxID=2:
RN [1]
RP NUCLEOTIDE S:
RC STRAIN=NCC 2
RX MEDLINE=2229
RA Pessi G., Zw
RA Pessi G., Zw
RA Pridmore R.D
RT "The genome
RT to the human
RL Proc. Natl.
DR GO; GO:00043
DR GO; GO:00043
DR GO; GO:00061
DR GO; GO:00061
DR GO; GO:00061
DR InterPro; IF
DR Fam; PF0069
DR Pfam; PF0010
DR Pfam; PF00157
DR Pfam; PF0306
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Nature 430:35-44(2004).

R EMBL; CR382139; CAG90360.1; -; Genomic_DNA.

R Interpro; IPR001680; WD40.

R PF00400; WD40; 6.

R PROSITE; PS50294; WD_REPEATS_REGION; 1.

Complete proteome; Repeat, WD_repeat.

Complete proteome; Repeat, WD_repeat.
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     to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (20
EMBL; AE014295; AAN25329.1; -; Genomic_DNA.
HSSP; P25715; 1MLA.
GO; GO:0005835; C:fatty acid synthase complex;
GO; GO:0004312; F:fatty-acid synthase activity;
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR004136; 2nprop_dioxygen.
InterPro; IPR001227; Ac_transferase.
InterPro; IPR003965; Fatty_acid_synth.
InterPro; IPR002539; MaoC_dehydratas.
Pfam; PF00698; Acyl_transf_1; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
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[1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=NCC 2705;

MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pn

Schell M.A., Karmirantzou M., Snel B., Vilanova D

Pessi G., Zwahlen M.-C., Desiere F., Bork P., Del

Pridmore R.D., Arigoni F.;

"The genome sequence of Bifidobacterium longum re
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Bifidobacterium longum.
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Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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B., Vilanova D.,
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Lalia Gammaproteobacteria; Pseudomonadales;

**SEQUENCE.*

**ALISACCC 15692 / PAO1;

**MEDLINE=2043737 PubMed=1094043; DOI=10.1038/35023079;

**RA Hicky M.J. Brinkman F.S. L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

**RA Hicky M.J. Brinkman F.S. L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

**RA Garber R.L., Goltry L., Tolentino E., Westbyck-Wadman S., Yuahr Y.,

**RA Bridy L.L., Coulter S.N., Polger K. R., Kas A., Larbig W. Lim R.M.,

**RA Bridy L.L., Coulter S.N., Polger K. R., Kas A., Larbig W. Lim R.M.,

**RA Bridy L.L., Coulter S.N., Polger K. R., W. Z., Pauleen I. T.,

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; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
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RESULT 15
Q4ZUU5_PSESY
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AC Q4ZUU5;
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RC STRAIN=B728a;

RC Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,

AN ADJAN M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,

AN ADJAN M., Richardson P.M., Kyrpides N.C., Ivanova N.;

"Comparison of two complete genome sequences of Pseudomonas syringae

RT pv. syringae B728a and pv. teomato DC3000.";

RP PYCO. Natl. Acad. Sci. U.S.A. 0:0-0(2005).

RR PYCO. Natl. Acad. Sci. U.S.A. 0:0-0(2005).

RR STRAIN=B728a;

Loper J.;

Loper J.;

RR SUBmitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

RR STRAIN=B728a;

RR SUBmitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

RR STRAIN=B728a;

RR SUBMITTED (MAY-2005) to the EMBL/GenBank/DDBJ databases.

RR InterPro; IPR006315; AutoCtransporter.

RR InterPro; IPR00499; Pertactin_C.

RR Ffam; PF03127; Pertactin_C.

RR RRINTS; PR01404; PRTACTNPAMLY.

RR RRINTS; PR01404; PRTACTNPAMLY.

RR SIGNAL

1 32 Potential

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RG STRAIN=B728A;

RC STRAIN-B728A;

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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Outer membrane autotransporter barrel precursor.
ORFNames=Psyr_2034;
Pseudomonas syringae pv. syringae B728a.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=205918;
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Sporidiobolus
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N-PSDB; AAH74580.
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                              Disclosure;
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The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequences given in ABQ81843. Also described is a polynucleotide (II) encoding a fusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from tablets, liquid bacterial based products, milk based products, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detect identification; lactic acid bacterium; diarrhoea; pathogenic rotavirus; food composition; pharmaceutical composition.
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                                                                                                                                                                                                                                              A thermostable DNA ligase from a hyperthermophilic archaebacterium, e.g. P. furiosus, catalyses template-dependent ligation at temps. of 30-80 degrees C, and retains its catalytic ability when subjected to temps. of 85-100 degrees C. The ligase functions effectively in the ligase chain reaction without significant blunt-end ligation. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA ligase from specificity and stability at in ligase chain reaction.
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N-PSDB; AAQ55729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3172 AA;
                                            IPDNAVLEGSLVKVTGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIPDNAVLEGSLVKVTGANG 20
IPEKAIVEGELVAI-GENG 307
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                                                                                      49.5%; ilarity 52.6%; Conservative
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larity 50.0%;
Conservative
                                                                                                                                                                                     AA;
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(first entry)
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                                                                                                                                                                                                                                 field.)
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                                                                                                                                                                                                                                                                                                                                                                                         84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schoettlin
                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                            20
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Pred. No. 1.5e+02;
; Mismatches 6
                                                                                                             Score 48.5;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus - has improved ligation high temperatures, giving greater efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
A
                                                                                          Mismatches
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                                                                                            Indels
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                                                                                                                                        561;
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RESULT 9
AAR96967

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RESULT 10
ABU37839
ID ABU37
XX
AC ABU37
XX
DT 19-JU
XX
DE Prote
XX
COS Prote
XX
OS Neise
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PN WO200
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PD 03-O0
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                       Plasmid cor reactions,
                                                                                                                                                                                                                                                                                                                                             WPI; 199
                                                                                                                                                                                                                                                     The present sequence is that of a purified thermostable DNA ligase isolated from a hyperthermophilic marine archaebacterium, Pyrococi furiosus (Pfu). The Pfu DNA ligase catalyses template dependent list temperatures of about 30-80 deg.C, and substantially retains it catalytic ability when subjected to temperatures of 85-100 deg.C. an estimated mol. wt. of 50-70 kDa. (Updated on 25-MAR-2003 to co.
                                                                                                                                                                                                                                                                                                                                                                                                                                               US5506137-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus
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LCR; template
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26-SEP-1996
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                                                                                                                                                                                                                                             an estimated mol. field.)
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                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                               ABU37839
                                                                                                                              ABU37839
                                                                                                                                                                                                                              Sequence
                                                                                                19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                    (STRA-)
                                                                                  Protein
        21-MAR-2002;
                        03-OCT-2002
                                      WO200277183-A2
                                                    Neisse
                                                                   Antisense;
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)B; AAT14926.
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18, stable u
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10; Conser
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                                                    meningitidis
                                                                   prokaryotic
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         2002WO-US009107
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No.
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34;
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                                                                                  gene
                                                                                                                                                                                                                                                                                                                               ligase
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                                                                    proliferation;
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RESULT 11
ADX95802
ID ADX95
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AC ADX95
XX
DT 21-AF
XX
DE Plant
XX

ADX95802;

21-APR-2005

entry)

Plant

length

insert polypeptide segid 58466

RESULT

ADX95

802

18

andard;

protein; 947 AA.

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268

PDNRLMSADIEGKTVMVTGAGG 289

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                                                                                                                                           the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that that an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) manufacturing an antibiotic; (10) profiling a compound that influences the activity of pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the penetral proliferation to isolate candidate molecules for rational for cellular proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, cellular prolaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained cellular prolaryotic essential genes. Note: The sequence data for this patent did not form part of the present sequence is encoded by one of the patent did not form part of the present sequences.
                                           Query Ma
Best Loo
Matches
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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N-PSDB;
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Wall
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                                            Similarity
12; Conserv
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Trawick JD,
- PD
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                                          49.0%;
nilarity 54.5%;
Conservative
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2001US-00948993.

2001US-0342923P.

2002US-00072851.

2002US-0362699P.
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         N----AVLEGSLVKVTGANG
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Carr GJ,
                                                   Score 48; DB Pred. No. 49; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R, Yamamoto R,
            20
                                                 Mismatches
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                                                                                    Length 636;
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Xu HH;
                                                   Gaps
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RESULT 12
ADY22708
ID ADY22708
XX
AC ADY22708;
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                                                                                                                                                                                                                         Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant cold, heat, drou pests, for confe improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant recombinant DNA construct; physical array; plant breeding cold tolerance; heat tolerance; drought tolerance; herbici extreme osmotic condition; pathogen tolerance; pest tolera growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth yield; plant growth; plant development; seed oil; protein protein content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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(KOVA/)
(SCRE/)
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(CAOY/)
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                                                                                                                                                                                                                                                                                                        Sequence
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05-NOV-2001;
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                                                                                                                                                                                                                        th 49.0 Similarity 55.6 10; Conservative
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                                                                                                                                                                                                                                                                                                           947
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                                            standard;
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2001US-00985678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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lant breeding marker;
rance; herbicide toler
; pest tolerance;
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The invention describes a recombinant DNA construct comprising a construct comprising a construct comprising a construct comprising a consilection are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for comproving plant tolerance to cold, heat, drought, herbicides, extreme comprision or plant cells by modification of the cell cycle pathway, for conferring confinence to plant disease, for producing galactomannan, construct is useful for increased resistance to plant disease, for producing galactomannan, confining or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypetide that can be used in the recombinant DNA construct of the
Query Ma
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                                                                                   content. This polypeptide tinvention.
                                                                                                                                                                                                                                                                                                                                                                                  pests, for improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                cold,
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(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
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05-NOV-2001
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                                                       Sequence
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               Local
                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                recombinant DNA construct, useful for improving plant tolerance to d, heat, drought, herbicides, extreme osmotic conditions, pathogens ts, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2004-18
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Simi
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou
                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                        965
                                                                                                                                                                                                                                                                                                                                                                                   yield.
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49.0%;
larity 55.6%;
Conservative
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                                                          AA;
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2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide
Score 48; DB Pred. No. 80; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SE,
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6
                             Length 965;
   Indels
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ABO69084
ABO69084
ABO69084
ABO69084
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ABO69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides encoding them. The sequences are useful in diagnosis and the prophylaxis and treatment of pathological conditions, as molecular targets for diagnosis and cc prophylaxis and treatment of pathological conditions resulting from a cc bacterial infection, for evaluating a compound, such as a polypeptide, cfor the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of p. aeruginosa-derived peptides or polypeptides, as target infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CABO84396 represent P. aeruginosa polypeptides of the invention. Note: The specification but was obtained in electronic format from USPTO at sequence.html
                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                           Query Ma
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding Pseudomonas aeruginosa puseful as molecular targets for diagnostics, prophylaxis and pathological conditions resulting from bacterial infection.
                                                                                                                                                          LT 14
1869
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N-PSDB; ABD02655.
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                               19-JUN-2003
      Protein
                                                                                             ABU39869
                                                                                                                                        ABU39869
                                                                                                                                                                                                                                                                                                                                                                    Local
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Similarity 55.6%;
O; Conservative
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                                                                                                                                          standard;
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8US-0094190P
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                                                                                                                                      protein;
      Prokaryotic
                                                  entry)
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Pred. No. 94
1; Mismatche
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       essential
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                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O
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94;
hea
     gene
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                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                             Length 802;
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1 treatment of
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Conservative

/ Match Local S

Similarity

48.0%;

Score 47; DB Pred. No. 1.1e 2; Mismatches

1.1e+03; DB 6;

Length 6310;

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Indels

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression controlled and inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated containing the vector; (4) an isolated containing the vector; (6) antibited by the inding continuation or the formal through the proliferation of the sequence of the gene product or that has an activity against (6) inhibiting cellular proliferation; (8) containing the vector of an antibiody capable of specifically binding containing the vector of an antibiody capable of specifically binding containing an activity against a biological pathway of the gene product of the test compound that inhibits proliferation; (8) compound acts; (9) manufacturing an antibiotic; (10) profiling a compound acts; (12) manufacturing an antibiotic; (10) profiling a compound acts; (12) dentifying an antibiotic; (10) profiling a compound acts; (11) a culture compound that inhibits the gene product its overexpersed or underexpressed; (12) determining the extent convents of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of solate candidate molecules for rational convents of properame, or for screening for homologous nucleic acids are useful for cequired for proliferation in cells other than S. aureus, S. typhimurium, ce patent did not form at directly from WIPO at the sequence data for this in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; S
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Sequence
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SDB; ACA4
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Trawick JD,
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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Carr C
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Forsyth RA,
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Xu HH;
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ABG28376
ID ABG28
ABG28376
ID ABG28
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XX ABG28
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KW Homo
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                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal contivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food guplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                      Query Match
Best Local
Matches 1
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                                                                                                                                                                                                                  Sequence
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N-PSDB; AAS92563.
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23-AUG-2000;
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PCT-US93-06939-1
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REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                      Sequence 1, Application PC/TUS9306939 GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5
CURRENT APPLICATION DATA:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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ORGANISM: Pyro
                                                                                                          APPLICANT: Eric J. Mat
APPLICANT: Edward J. M
APPLICANT: Warren E. S
TITLE OF INVENTION: Pu
TITLE OF INVENTION: Py
TITLE OF INVENTION: Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pyrococcus INDIVIDUAL ISOLATE: I CELL TYPE: unicelluls IMMEDIATE SOURCE:
ZIP: 94111
COMPUTER READABLE
                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: lincollecure
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916-232-1
                                   STREET:
CITY: 5
STATE:
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California
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DABLE FORM:
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ISOLATE: DSM #3638
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RESULT 7
US-09-252-991A-17830
; Sequence 17830, Application US/09252991A
parent No. 6551795
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US-09-252-991
                                              Query Ma
Best Loc
Matches
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17830
LENGTH: 802
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Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/FILING DATE: 1000

CLASSIFICATION 1000
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Best Local
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ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,22
REFERENCE/DOCKET
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PRIOR APPLICATION
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                                                                                                                           TYPE:
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ORIGINAL SOURCE:
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INDIVIDUAL
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ON FOR SEQ ID NO:
E CHARACTERISTICS:
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E/DOCKET NUMBER: STRICATION INFORMATION:

3: (415) 433-4150

(415) 433-8716
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L ISOLATE: DSM #3638
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Sequence 16593, Application US/09248796A; Patent No. 6747137; GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMING
TITLE OF INVENTION: FOR DIAGNOSTICS AND T
FILE REFERENCE: 107196.132;
CURRENT APPLICATION NUMBER: US/09/248,796A;
CURRENT FILING DATE: 1999-02-12;
PRIOR APPLICATION NUMBER: US 60/074,725;
PRIOR APPLICATION NUMBER: US 60/074,725;
PRIOR APPLICATION NUMBER: US 60/096,409;
PRIOR FILING DATE: 1998-08-13;
NUMBER OF SEQ ID NOS: 28208;
SEQ ID NO 16593;
LENGTH: 308
TYPE: PRT
ORGANISM: Candida albicans
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APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Pol

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2830P1C23

CURRENT APPLICATION NUMBER: US/10/012,231A

CURRENT FILING DATE: 2002-06-10

Prior Application removed - See File Wrapper or Pa

NUMBER OF SEQ ID NOS: 477
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                                                                                                                                                         SEQ ID NO 116
LENGTH: 331
TYPE: PRT
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sequence 16593, Application US/09248796A
Patent No. 6747137
                                                                                                                           ORGANISM: Homo
10-012-231A-116
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                                                                                                                                            ORGANISM:
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Similarity 52.6%;
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Botstein, David
Desnoyers, Luc
Eaton, Dan 1.
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RESULT 10
US-10-015-389A-116
; Sequence 116, App
; Sequence 16, App
                                         APPLICANT: Hillan, APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Point Invention: Acids Encoding the Same
FILE REFERENCE: P2830P1C10
CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
CURRENT FILING DATE: 2002-03-05
CURRENT OF SEQ ID NOS: 477
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US-10-006-768A-11
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US-10-006-768A-11
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                     NUMBER OF SEQ I
Prior Applicati
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
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CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C48
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
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R;She, Q.; Singh, R.K.; Confalonieri
Jong, I.; Jeffries, A.C.; Kozera, C.
arrett, R.A.; Ragan, M.A.; Sensen, C.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricu
A;Reference number: A99139
A;Accession: D90218
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <KUR>
A;Cross-references: UNIPROT:Q9UX91; UN
C;Genetics:
A;Gene: rp16AB
C;Superfamily
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DB5608
hypothetical protein Z1183 [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Accession: D85608; E85659
C;Accession: D85608; E85659
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E. Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Residues: preliminary
A;Rolecule type: DNA
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Rosecule type: DNA
A;Residues: 1-111 <ST2>
A;Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:91
A;Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:91
A;Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:91
A;Genetics:
A;Genet Z1183; Z1622
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D90218
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revisio
C;Accession: D90218
R;She, Q.; Singh, R.K.; Confalonieri,
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A;Molecule type: DNA
A;Residues: 1-778 <KUR>
A;Cross-references: UNIP
C;Genetics:
A;Gene: AGR C 1799
A;Map position: circular
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C.; Kozera, C.J.;
N.; Sensen, C.W.;
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                                                      UNIPARC: UPI000013416E;
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anta, E.;
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A32687; MUID: 9062204; PMID: 2684982
A;Reference number: A32687; MUID: 90062204; PMID: 2684982
A;Reference number: A32687; MUID: 90062204; PMID: 2684982
A;Reference number: A32687; MUID: 90062204; PMID: 2492988
A;Reference number: A32687; MUID: 90062204; PMID: 2492988
A;Reference number: A32687; MUID: 90062204; PMID: 2684982
A;Reference number: A32687; MUID: 90062204; PMID: 2684982
A;Residues: 1-653 < CHA>
A;Residues:
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H70326
hypothetical protein aq 294 - A
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_r
C;Accession: H70326
R;Deckert, G.; Warren, P.V.; Ga
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A;Accession: H70326
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Residues: 1-371 <AQF>
A;Residues: 1-371 <AQF>
A;Cross-references: UNIPROT:066644; UNIPARC:UPI00000562FF; GB:AE000682; A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_294
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probable 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) [i C;Species: Sinorhizobium meliloti
C;Oate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_chang
C;Accession: D95957
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, F.
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb p5ymB megaplasm
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95957
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-254 <KUR>
A;Cross-references: UNIPROT:092V10; UNIPARC:UPI00000CB6D2; GB:
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Feder
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Ki
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Well
A;Title: The composite genome of the legume symbiont Sinorhizc
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Genome: plasmid
C;Superfamily: short-chain dehydrogenase; short-chain alcohol
C;Keywords: oxidoreductase
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hypothetical protein T28I19.100 - Ara C; Species: Arabidopsis thaliana (mous C; Date: 30-Apr-1999 #sequence_revision C; Date: 30-Apr-1999 #sequence_revision C; Date: 30-Apr-1999 #sequence_revision C; Date: 30-Apr-1999 #sequence_revision C; Accession: T06029
A; Reference number: Z15484
A; Reference number: Z15484
A; Residues: 1-532 <BEV>
A; Cross-references: UNIPROT: Q9T069; UA; Experimental source: cultivar Column C; Genetics:
A; Gene: ATSP:T28I19.100
A; Map position: 4
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RESULT

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Search completed Job time: 19.33

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probable alcohol dehydrogenase (EC 1.1.1.) [similarity] - Caenorhal C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-C;Accession: T33939
R;Becker, M.; Graves, T.; Wilson, C.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid D2063.
A;Reference number: Z21442
A;Accession: T33939
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-408 <BEC>
A;Cross-references: UNIPROT:Q9UAT1; UNIPARC:UPI00000762B1; EMBL:AF1
A;Experimental source: strain Bristol N2; clone D2063
C;Genetics:
A:Gene: CESP:D2063.1
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A;Map position: 5
A;Introns: 294/3; 359/3; 373/3
C;Superfamily: alcohol dehydrogena
C;Keywords: NAD; oxidoreductase; z
F;47,70,173/Binding site: zinc, ca
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A; Reference number
A; Accession: A6941
A; Status: prelimin
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A;Molecule type: D
A;Residues: 1-501
A;Cross-references
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A; Reference number: A69250; MUID:98049343; PMID:9389475

A:Status
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ilarity 45.0%;
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4; Mismatches
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LENGTH: 331
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
Prior application removed - See File Wrapper ON NUMBER OF SEQ ID NOS: 477
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2830P1C46
CURRENT APPLICATION NUMBER: US/10/01
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Fong, Sherman
Gao, Wei-Qiang
                                                                     Eaton, Dan 1.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
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Hillan, Kenneth J.
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APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pann, James
APPLICANT: Pann, James
APPLICANT: Pann, James
APPLICANT: Pann, James
CURRENT: Pann, James
APPLICANT: Pann, James
CURRENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C2
CURRENT APPLICATION NUMBER: US/10/011,833A
CURRENT APPLICATION NUMBER: US/10/011,833A
CURRENT APPLICATION Temoved - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-011-833A-116
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US-10-011-833A-116
; Sequence 116, Ap
; Patent No. 69519
; Patent No. 69519
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US-10-006-041A-116
; Sequence 116, Applicate  
; Patent No. 6951921
; GENERAL INFORMATION:
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Similarity 52.6%;
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Botstein, David
Desnoyers, Luc
Eaton, Dan 1.
Ferrara, Napoleo
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J
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Desnoyers, Luc
Eaton, Dan 1.
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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ID NOS: 477
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APPLICANT

Paul J.

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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1CB
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 116
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-041A-116
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Search completed: March 11, Job time : 28.3016 secs
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Best Local Similarity 52.6%;
Matches 10; Conservative
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Sequence 20893, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION: APPLICANT: Alexandrov, Nickolai et al. TITLE OF INVENTION: Sequence-Determined DNA FrITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2; CURRENT APPLICATION NUMBER: US/11/096,568A; CURRENT FILING DATE: 2005-04-01; NUMBER OF SEQ ID NOS: 34471; SEQ ID NO 20893; LENGTH: 277
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US-11-096-568A-20894
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US-11-096-568A-20893
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Similarity 28.9%;
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ilarity 57.1%;
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US-11.
; Sequence 1266, ...;
; Publication No. US2006UU---;
; Publication No. US2006UU---;
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Francisco FILLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
CURRENT FILING DATE: 2005-04-01
                                              ; FEATURE:
; NAME/KEY: mis
; LOCATION: (1)
; OTHER INFORMA
US-11-096-568A-12
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US-11-096-5
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US-11-096-568A-1266
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SEQ ID NO 1267
LENGTH: 246
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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NAME/KEY: mis
LOCATION: (1)
OTHER INFORMA
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INFORMATION: Cer
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Similarity 57.9%;
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US20060048240A1
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Pred. No. 24;
1; Mismatches
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Score 41.5; D
pred. No. 29;
1; Mismatches
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; TYPE: PRT; ORGANISM: Zea mays subsp; FEATURE: ; NAME/KEY: misc_feature; LOCATION: (1)...(316); OTHER INFORMATION: Ceres US-11-096-568A-1265
RESULT 14
US-11-087-099-4990
; Sequence 4990, Application US/11087099
; Publication No. US20060041961A1
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US-11-052-554A-211
; Sequence 211, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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US-11-096-568A-1265
; Sequence 1265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
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SEQ ID NO 211
LENGTH: 1562
TYPE: PRT
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Best Local S
Matches 10
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Matches 11
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FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1265
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11-052-554A-211
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Similarity 52.6%;
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Similarity 57.9%;
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Pred. No. 2.3e
3; Mismatches
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Pred. No. 33;
1; Mismatches
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RESULT 15
US-11-096-568A-12932
; Sequence 12932, Application No. US2000; Publication No. US2000; GENERAL INFORMATION:
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US-11-087-099-499
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TITLE OF INVENTION: Genes and Uses for Plan;
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099;
CURRENT FILING DATE: 2005-03-22;
NUMBER OF SEQ ID NOS: 12464;
SEQ ID NO 4990;
LENGTH: 175
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SEQ ID NO 12932
LENGTH: 234
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TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                              LOCATION: (1). (234)
OTHER INFORMATION: Ceres
11-096-568A-12932
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NAME/KEY: misc
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US-10-989-488A-
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US-10-437-963-171580
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APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR
FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/989,4
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR
FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/989,
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR FILING DATE: 2000-12-08
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SEQ ID NO 35
SEQ TH: 343
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SEQ ID NO 37
LENGTH: 343
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                                                  Sequence 171580, Application US Publication No. US20040123343A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn ve
APPLICANT:
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APPLICANT:
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APPLICANT: Bui, Pe
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TYPE: PRT
ORGANISM:
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OTHER
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ORGANISM: Artificial
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Similarity 81.8%;
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   Kovalic, bu.
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ilarity 81.8%;
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RESULT 10
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SEQ ID NO 17158(
LENGTH: 279
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Best Local S
Matches 10
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CURRENT APPLIC
CURRENT FILING
PRIOR APPLICAT
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT:
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                 SOFTWARE:
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OTHER INFORMATION:
0-437-963-171580
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                                                                                                              REPERENCE: ELITRA.034A
RENT APPLICATION NUMBER: US/10/282,122A
RENT APPLICATION NUMBER: US/10/282,122A
RENT FILING DATE: 2003-02-20
OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
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ning Prior App
R OF SEQ ID NO
NARE: PatentIn
NO 65763
                                                                          FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
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Malone, Cheryl
Haselbeck, Robe
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Rober
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ilarity 62.5%;
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yskind, Judith
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Pred. No. 6.9;
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APPLICANT: Zhou, Yihua;
APPLICANT: Cao, Yongwei;
TITLE OF INVENTION: Nucleic Acid N
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 273937
LENGTH: 892
TYPE: per
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US-10-425-115
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                                                                                                                                                                                                                                                            RESULT 12
US-10-425-114-58466
                                                                                                            APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Au
FILE REFERENCE: 70
                                                Query Match
Best Local S
Matches 10
                                                                   NUMBER OF
SEQ ID NO 5
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Sequence 273937, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Value
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LOCATION: (1)..(892
OTHER INFORMATION: (FEATURE:
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10-425-115-
                                 LENGTH: 94
TYPE: PRT
ORGANISM:
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ORGANISM:
OTHER INFORMATION: 0-425-114-58466
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APPLICANT: Carr, CAPPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
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US-10-425-114-70492
US-10-425-114-70492, Application
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Best Local
Matches 1
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Best Local
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70492
LENGTH: 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67793, Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Zhou, Yihua
Kovalic, David K.
Screen, Steven E
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Trawick, John
Carr, Grant
Yamamoto, Ro
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Malone, Cheryl
Haselbeck, Rober
Ohlsen, Kari
Zyskind, Judith
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US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                      Robert
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Pred. No.
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data remove NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67793
LENGTH: 6310
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-67793
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: NOVEL NUCLEIC ACIDS AND PO
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
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US-10-450-763-58735
; Sequence 58735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
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                                                                                                                                            GRGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (92)..(104)
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain
OTHER INFORMATION: identified by eMATRIX, accession number PR00081B, p-va
OTHER INFORMATION: 11, raw score of 10.38
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(131)
OTHER INFORMATION: short chain dehydrogenase domain identified by PFam,
OTHER INFORMATION: accession name adh_short, E-value=9.1e-05, PFam score
US-10-450-763-58735
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Matches 10
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SOFTWARE: Custom
SEQ ID NO 58735
LENGTH: 133
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12; Conservative
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ACPSKATIPGKTVIVTGAN
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Pred. No. 1.3e+03;
2; Mismatches 6;
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                                                                         Score 46; DB Pred. No. 19; Mismatches
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Search completed: March 11, 2006, 05:16:12 Job time : 97.3333 secs

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GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
APPLICANT: Edward J. Marsh
APPLICANT: Edward J. Marsh
APPLICANT: Warren E. Schoettlin
TITLE OF INVENTION: Purified Thermo
TITLE OF INVENTION: Pyrococcus Furi
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
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REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acide
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Best Local S
Matches 10
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CLONE: p
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MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-D

SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: proto
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 07/9
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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   COMPUTER
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CLASSIFICATION:
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                                                                                            CITY:
STATE:
                                                           COUNTRY:
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: California
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Similarity 52.6%;
10; Conservative
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2730 Sand Hill Road
enlo Park
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2001 Ferry Building
n Francisco
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Edward J. Marsh
Warren E. Schoettlin
Warren Warren E. Schoettlin
Warren 
                                                                USA
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Pred. No. 7
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Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO FITTLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17830
LENGTH: 802
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US-09-252-9
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PCT-US93-06939-1
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                                                                                                             ; ORGANISM: Pseudomonas US-09-252-991A-17830
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Patent No
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Matches 10
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FILING DATE: July 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: STRG 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEFAX: 278356
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FORIGINAL SOURCE:
ORGANISM: Pyro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
IMMEDIATE SC
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3+ inch, COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 561 amino acids
TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHA
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PRIOR APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pyrococcus Furiosus INDIVIDUAL ISOLATE: DSM #3638 CELL TYPE: unicellular organism
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o. 655
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ilarity 52.6%;
Conservative
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                           NAVLEGSLVKVTGANG 21
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3, 1992
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 481
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RESULT 9
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US-08-849-602C-
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                                                                                                                                                                                   Patent No. 5248599
APPLICANT: SAKIYAMA, FUMIO; NAKATA,
TITLE OF INVENTION: ACHROMOBACTER
PRODUCT THEREOF
                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Fabricius, Helle
APPLICANT: Hastrup, Sven
TITLE OF INVENTION: A Process o
TITLE OF INVENTION: Extracellul
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61718230 No. 6
                                               Query Match
Best Local S
Matches 11
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Best Local S
Matches 11
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FABLSEQ for Windows Version:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,602C
FILING DATE: 02-JUN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4139.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                           08-849-602C-27
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: sin
                                                                                                              LENGTH:
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CITY: New
STATE: NY
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                                              1 45.1%;
Similarity 52.4%;
L1; Conservative
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Similarity 52.4%;
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Pred. No. 20;
4; Mismatches
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Sequence 16593, Application US/09248796A; Patent No. 6747137; GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACTITLE OF INVENTION: FOR DIAGNOSTICS AND THER FILE REFERENCE: 107196.132; CURRENT APPLICATION NUMBER: US/09/248,796A; CURRENT FILING DATE: 1999-02-12; PRIOR APPLICATION NUMBER: US 60/074,725; PRIOR APPLICATION NUMBER: US 60/074,725; PRIOR APPLICATION NUMBER: US 60/096,409; PRIOR FILING DATE: 1998-02-13; PRIOR FILING DATE: 1998-08-13; NUMBER OF SEQ ID NO 16593; LENGTH: 308; TYPE: PRT
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US-09-248-796A-16593
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                                                                                                                  NUMBER OF SEQ
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Home
S-10-012-231A-11
                                                        Query Match
Best Local S
Matches 10
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APPLICANT: Baker, K
APPLICANT: Botstei
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APPLICANT:
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                                                                                                                                                                                         APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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Gao, Wei-Qiang
Goddard, Audrey
                           AIPDNAVLEGSLVKVTGAN 20
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|PDNILDAFSLKGKVASVTGSSG 73
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
                                                                                                                                                                                                                                                                                                             Pan, James
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                                                        44.7%;
ilarity 52.6%;
Conservative
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ilarity 43.5%;
Conservative
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ton, Dan 1.
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                                                       Score 46; DB Pred. No. 11; Mismatches
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Pred. No.
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Mismatches
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TITLE OF INVENTION: Secreted and Transmembrane Po-
TITLE OF INVENTION: Secreted and Transmembrane Po-
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C48
CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
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US-10-015-389A-116
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US-10-006-768A-116
                                                                               APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Pan, James

APPLICANT: Pan, James

TITLE OF INVENTION: Secreted and Transmembrane Po

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2830P1C10

CURRENT APPLICATION NUMBER: US/10/006,768A

CURRENT FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 477
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Matches 10
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GENERAL INFORMATION:
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                                          Prior Application removed SEQ ID NO 116 LENGTH: 331
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APPLICANT:
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ORGANISM: Homo
0-006-768A-116
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Botstein, David
Desnoyers, Luc
Eaton, Dan l.
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
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Pan, James

TITLE OF INVENTION: Secreted and Transmembrane Po.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
Prior application removed - See File Wrapper or Prior Application removed - See File Wrapper or Number Of SeQ ID NO 116
LENGTH: 331
TYPE: PRT
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US-10-015-393A-116
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APPLICANT: Hillan, Newwood APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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Botstein, David
Desnoyers, Luc
Eaton, Dan 1.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
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Ferrara, Napoleone
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Goddwski, Paul J.
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CURRENT APPLICATION NUMBER: US/10/015,393A; CURRENT FILING DATE: 2002-06-10; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 477; SEQ ID NO 116; ENGTH: 331; TYPE: PRT; ORGANISM: Homo sapiens
US-10-015-393A-116
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Search completed: March 11, Job time: 28.6667 secs
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N-PSDB; AAH74580.
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The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide casequences given in ABQ81842 and ABQ81843, or a sequence given in C least 90% identity or which hybridises with the sequences given in C ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a C fusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a C heterologous polypeptide. (I) has antidiarrheic and antibacterial C activities, and can be used as an inhibitor of Salmonella. (I) (which is C a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, cheese, fermented milks, milk based fermented powders, infant formula, pet food or a pharmaceutical composition selected from tablets, piquid bacterial suspensions, dried oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the carpression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bactrotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of preparing high yields of an (R) hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II used in the method of the invertence.
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Similarity 81.8%;
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                                                                                                                                                                                                                                      A thermostable DNA ligase from a hyperthermophilic archaebacterium, e.g. P. furiosus, catalyses template-dependent ligation at temps. of 30-80 degrees C, and retains its catalytic ability when subjected to temps. of 85-100 degrees C. The ligase functions effectively in the ligase chain reaction without significant blunt-end ligation. (Updated on 25-MAR-2003)
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larity 50.0%;
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Pred. No. 38;
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RESULT 9 AAR96967

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                        Claim
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                                                          Neisseria
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PIXPR
                           the invention relates to an isolated nucleic acid comprising any one of the scall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway or a gene on which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational compound that inhibits the present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Forsyth RA,
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RESULT 12
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larity 55.6%;
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                                                                                                                                                                                                                             Schistcooma mansoni protein, or its portion which is at least 20 amino cacids in length. Also included are an expression vector comprising the nucleic acid operably linked to a promoter, a recombinant cell transformed/transfected with the nucleic acid (or expression vector), an immunogenic composition comprising the nucleic acid in combination with a comprising an amino acid sequence encoded by the nucleic acid, an immunogenic composition comprising the isolated S. mansoni protein continuous which specifically binds to the isolated S. mansoni protein, an immunogenic composition comprising the isolated S. mansoni protein, an immunogenic composition comprising the isolated S. mansoni protein, an immunogenic composition in specifically binds to the isolated S. mansoni continuous and comprising the isolated S. mansoni protein, an immunogenic composition infection in a subject and a computer readable medium having recorded in it a nucleic acid molecule from S. C. mansoni genome. The nucleic acid molecule is useful for preventing, and composition in the nucleic acid molecule from S. C. diagnosing, or treating S. mansoni infection (schistosomiasis). It can send be used as vaccine against S. mansoni. The present sequence is a contained in electronic form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from WIPO at firsting.

It is included in the specification but are not included in the sequence
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140
                                                                                      10; Conservative
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Garcia JCL, N
, Setubal JC,
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C, Menck
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4; Mis
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Madeira
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Nascimento ALTO;
AMBN, Rodrigues
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ABU39869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Pseudomonas aeruginosa polypeptides and the golynucleotides encoding them. The sequences are useful in diagnosis and the therapy of pathological conditions, as molecular targets for diagnostics, grophylaxis and treatment of pathological conditions resulting from a component infection, for evaluating a compound, such as a polypeptide, growing anti-P. aeruginosa nucleic acid, as components of including anti-P. aeruginosa drugs, as targets for antibacterial drugs, components for diagnosis and/or treatment of P. aeruginosa-derived peptides or polypeptides, as target infection, and in detection of P. aeruginosa sequences or other sequences infection, and in detection of P. aeruginosa sequences or other sequences in patent in this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed in sequences obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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N-PSDB; ABDO
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27-JUL-1998;
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                                                                                                                                                                               protein;
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Pred. No. 1e+02;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits proliferation or the biological pathway in which a proliferation and that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous mucleic acids are useful for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous mucleic acids are useful for identifying proteins or screening for homologous mucleic acids are useful for cequired for proliferation in cells other than 8. aureus, 8. typhimurium, 12 patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                            Query Match
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Matches 1
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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                                                                                                                                                                                                   Sequence
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N-PSDB; ACA43739.
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Similarity 37.5%;
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Trawick JD,
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                               Score 47; DB Pred. No. 1.2e 2; Mismatches
                                                -EGSLVKVTGANG
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Yamamoto R,
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Forsyth
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Search completed: Job time : 120.66 leted: March 11, 120.667 secs 2006, 05:02:25

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RESULT 9
US-10-437-963-171580
; Sequence 171580, Appl:
; Publication No. US200;
; GENERAL INFORMATION:
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TITLE OF INVENTION: SYNTHETIC GENES
FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/9
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/494,92
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/734,23
PRIOR APPLICATION NUMBER: 09/734,23
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/989, CURRENT FILING DATE: 2004-11-15 PRIOR APPLICATION NUMBER: 09/494,921 PRIOR FILING DATE: 2000-01-31 PRIOR APPLICATION NUMBER: 09/734,237 PRIOR FILING DATE: 2000-12-08 NUMBER OF SEQ ID NOS: 79
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LENGTH: 343
TYPE: PRT
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APPLICANT:
TITLE OF IN
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    APPLICANT:
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TITLE OF INVENTION: SYNTHETIC
FILE REFERENCE: B583:53896
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                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                          LENGTH: 343
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Similarity 88.9%;
6; Conservative
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                La Rosa, Thomas
Kovalic, David
Zhou, Yihua
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Zhou, Yinua
Cao, Yongwei
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US20050196774A1
                                                                    Application US, IS20040123343A1
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Pred. No. 0
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RESULT 10
US-10-282-122A-65
; Sequence 65763,
; Publication No.
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 171580
LENGTH: 279
Type: pro
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Best Local S
Matches 10
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ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone
3-10-437-963-171580
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Remaining Prior App
NUMBER OF SEQ ID NO
SOFTWARE: PatentIn
SEQ ID NO 65763
LENGTH: 636
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APPLICANT:
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APPLICANT:
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TITLE OF I
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                           PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                  DR APPLICATION NUMBER: 60/206,848
DR FILING DATE: 2000-05-23
DR APPLICATION NUMBER: 60/207,727
DR FILING DATE: 2000-05-26
DR APPLICATION NUMBER: 60/230,335
DR APPLICATION NUMBER: 60/230,335
DR APPLICATION NUMBER: 60/230,347
DR FILING DATE: 2000-09-09
DR APPLICATION NUMBER: 60/242,578
DR FILING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR APPLICATION NUMBER: 60/257,931
DR APPLICATION NUMBER: 60/267,636
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Boukharov, Andr
Barbazuk, Brad
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milarity 62.5%;
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Forsyth, R.
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                                                  Application data D NOS: 78614
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Pred. No. 6.4;
2; Mismatches
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                                                                     File
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RESULT 11
US-10-425-115-273937
; Sequence 273937, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
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US-
                                                                  APPLICANT: Zhou, Yihua;
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                             RESULT 12
US-10-425-114-58466
; Sequence 58466, Application US/
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid M
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 273937
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SEQ ID NO 5
LENGTH: 9
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(892)
OTHER INFORMATION: un
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10-282-122A-
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10-425-115-
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                          ORGANISM:
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Similarity 54.5%;
L2; Conservative
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Similarity 55.6%;
O; Conservative
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Pred. No. 80;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: US-10-425-114-70492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67793, Appli
Publication No. US200
GENERAL INFORMATION:
APPLICANT: Wang, Lia
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SEQ ID NO 7049
LENGTH: 965
TYPE: PRT
ORGANISM: Ze
FEATURE:
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GENERAL INFORMATION:
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APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70492
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APPLICANT:
APPLICANT:
                                                                                                                             APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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: Zhou, Yihua
: Kovalic, David K.
: Screen, Steven E
: Tabaska, Jack E
Yongwei
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Trawick, John
Carr, Grant
Yamamoto, Ro
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Haselbeck, Rober
Ohlsen, Kari
Zyskind, Judith
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alone, Cheryl
aselbeck, Robe
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RESULT 15
US-10-450-763-58735
US-10-450-763-58735
; Sequence 58735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
APPLICANT: HyBeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND INTITUDE OF INVENTION NUMBER: US/10/450,763
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILLING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUBtom
; SOFTWARE: CUBtom
; SEQ ID NO 58735
; LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data remove
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67793
LENGTH: 6310
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-67793
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                                                                                                                                                  NAME/KEY: DOMAIN
LOCATION: (92)..(104)
LOCATION: (92)..(104)
OTHER INFORMATION: identified by eMATRIX, accession number PR00081B, p-value=6.727e-
OTHER INFORMATION: 11, raw score of 10.38
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(131)
OTHER INFORMATION: short chain dehydrogenase domain identified by PFam,
OTHER INFORMATION: accession name adh_short, E-value=9.1e-05, PFam score of -12.5
-10-450-763-58735
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                                                                           Score 46; DB Pred. No. 18; 1; Mismatches
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Pred. No. 1.2e+03;
Pred. No. 1.2e+03;
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PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;

Rain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins Posker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S., A Posker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S., A Salzberg S., Saunders D., Seegar K., Sharp S., Rajandream M-A., Denning D.W., Barrell B., Hall N.;

"Insight into the genome of Aspergillus fumigatus: analysis of a 92 kb region encompassing the nitrate assimilation gene cluster."; kb region encompassing the nitrate assimilation gene cluster."; Fungal Genet. Biol. 41:443-453(2004).

R EMBL; BX649605; CAE47862.1; -; Genomic DNA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R InterPro; IPR001509; Epimerase_Dh.

R Pfam; PF01370; Epimerase; 1.

W Oxidoreductase.

SEQUENCE 352 AA; 39420 MW; 0E84223EEC87ABF9 CRC64;
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Matches 1
      Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,

A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.

Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,

A Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

A Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,

A Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,

A Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

A Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod

A Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,

Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
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Q4WSW9;
Q4WSW9;
13-SEP-2005 (TrEMBLrel. 31, Cre
13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
Aldehyde reductase II.
ORFNames=Afulg11360;
Aspergillus fumigatus Af293.
Eukaryota; Fungi; Ascomycota; P
Eurotiales; Trichocomaceae; mit
NCBI_TaxID=330879;
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Q6MYZ7_ASPFU PRELIMINARY; PRT; 352 AA.
Q6MYZ7;
Q6MYZ7;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q6MYZ7;
Q6MYZ7
Q6MYZ7
Q6MYZ7
Q6MYZ7;
Q6MYZ7
Q6
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mitosporic Trichocomaceae; Aspergillus.
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Best Local S
Matches 11
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Query Match
Best Local
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Q5ASZ7;
Q5ASZ7;
10-MAY-2005
10-MAY-2005
10-MAY-2005
Hypothetical
ORFNames=ANB
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Vassiliev H., Ven
Wu X., Wyman D.,
Lander E.;
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Eurotiales;
NCBI_TaxID=2
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EMBL; AACD01
Hypothetical
SEQUENCE 3
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Ronning C.M., Rutter S., Salzberg S.L., Sanchez M., Squares S., Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J. White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE
                                                                                                                                                    "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                 CAUTION:
EMBL/Ger
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                                                                                                                                  GenBank,
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                                                           ll protein.
341 AA; 37852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
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larity 50.0%;
Conservative
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ungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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                                                                                                                 data.
                                                                                                                               sequence shown here is derived
/DDBJ whole genome shotgun (WGS)
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39420 MW;
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  51.4%;
66.7%;
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; Pred. No. 5;
3; Mismatches
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Last sequence update)
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    Score
Pred.
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                                                             9381BB9083B3F9EA CRC64;
                                                                                               -; Genomic_DNA.
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     55; DB 2;
No. 13;
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                      Length 341;
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                                                                                                                                            which is
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                                                                                                                                                                                                                                                       Wilson B.
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Q4KBY7
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A Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson l

A Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovit;

A Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran l

A Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.,

T "Complete genome sequence of the plant commensal Pseudomonas

I Nat. Biotechnol. 23:873-878(2005).

R EMBL; CP000076; AAY95646.1; -; Genomic_DNA.

W Hypothetical protein.

SEQUENCE 398 AA: 4757.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

NCBI_TaxID=220664;

NCBI_TaxID
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Q4KK52_PSEF5 PRELIMINARY; PRT; 398 AA.
Q4KK52;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=PFL 0235;
Pseudomonas fluorescens (strain Pf-5).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=220664;
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KBY7 PSEF5

Q4KBY7 PSEF5 PRELIMINARY; PRT; 684 AA.

Q4KBY7;

13-SEP-2005 (TrEMBLrel. 31, Created)

13-SEP-2005 (TrEMBLrel. 31, Last sequence upda

13-SEP-2005 (TrEMBLrel. 31, Last annotation up

Phenylacetic acid degradation protein PaaN.

Name=paaN; ORFNames=PFL_3140;

Pseudomonas fluorescens (strain Pf-5).
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NUCLEOTIDE SEQUEN
STRAIN=Pf-5;
PubMed=15980861;
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12; Conservative
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; Gammaproteobacteria;
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RESULT 10
Q9RRV4 DEIRA
ID Q9RRV4;
AC Q9RRV4;
DT 01-MAY-2000 ('DT 01-MAY-2000 ('DT 01-JUN-2003 ('DE Aldehyde dehyde Aldehyde dehyde GN OrderedLocusNa OS Deinococcus rioc Deinococcus rioc Deinococcus rioc Deinococcus rioc NCBI TaxID=12 RN [1]
RN [1]
RP NUCLEOTIDE SERR NUCLEOTIDE SERR MEDLINE=20036 RA White O., Eist RA Moffat K.S., RA Wamathevan J., RA Makarova K.S., RA Ketchum K.A., RA Fraser C.M.; RT "Genome sequent RT" radiodurans R.
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Matches
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STRAIN=R;

Suzuki N., Okayama S., Nonaka H., Tsuge Y., Inui M.

"Large-Scale Engineering of the Corynebacterium glu

"Lappl. Environ. Microbiol. 71:3369-3372(2005).

EMBL; AB193033; BAD84061.1; -; Genomic DNA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002086; Aldehyd dehydrog.

InterPro; IPR002539; MaoC dehydratas.

InterPro; IPR011966; PaaN-DH.

Pfam; PF00171; Aldedh; 1.

Pfam; PF01575; MaoC dehydratas; 1.

TIGRFAMs; TIGR02278; PaaN-DH; 1.

SEQUENCE 698 AA; 75061 MW; E9781F184A0D8B57 CRO
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
Putative aldehyde dehydrogenase.
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium
NCBI_TaxID=1718;
                   NUCLEOTIDE SEQUENCE.
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Varchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
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RESULT 12
Q6WE60_PINMO
ID Q6WE60;
AC Q6WE60;
DT 05-JUL-2004 (TrEMBLrel. 27
DT 05-JUL-2004 (TrEMBLrel. 27
DT 05-JUL-2004 (TrEMBLrel. 27
DF putative NBS-LRR protein C
GN Name=RGA;
OS Pinus monticola (Western w
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ID Q6WES8 PINMO
ID Q6WES8;
AC Q6WES8;
DT 05-JUL-2
DT 
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EMBL; AE002069; AAF11927.1; -; Genomic_l

PIR; F75279; F75279.

TIGR; DR2381; -.

GO; GO:0016491; F:oxidoreductase activi:

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002086; Aldehyd_dehydrog.

InterPro; IPR002539; MaoC_dehydratas.

InterPro; IPR011966; PaaN-DH.

Pfam; PF00171; Aldedh; 1.

Pfam; PF01575; MaoC_dehydratas; 1.

TIGRFAM8; TIGR02278; PaaN-DH; 1.

Complete proteome.

SEQUENCE 700 AA; 75493 MW; E3F6FDA4
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PubMed=14586641; DOI=10.1007/s00438-003-0940-1;

Liu J.-J., Ekramoddoullah A.K.M.;

"Isolation, genetic variation and expression of gene analogs from western white pine (Pinus mont Don.).";

Mol. Genet. Genomics 270:432-441(2004).

EMBL; AY294116; AAQ57161.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006915; P:apoptosis; IEA.
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NON_TER
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
NCBI_TaxID=3345;
[1]
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MBL; AY294116; AAQ57161.1; -; mRNA.
D; GO:0005524; F:ATP binding; IEA.
D; GO:0006915; P:apoptosis; IEA.
nterPro; IPR002182; NB-ARC.
fam; PF00931; NB-ARC; 1.
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Similarity 63.2%;
12; Conservative
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Pred. No. 28;
2; Mismatches
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Pinus; Strobu
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RESULT 13
Q6WE61 PINMO
ID Q6WE61;
DC Q6WE61;
DT 05-JUL-2004
DC Putative NBS
GN Name=RGA;
OC Pinus montic
OC Spermatophyt
OX NCBI TaxID=3
RN [1]
RP NUCLEOTIDE S
RX PubMed=14586
RA Liu J.-J., E
RT "Isolation, E
RT "Isolation, E
RT "Isolation, E
RT "Gene analogs
RT Go; GO:00055
DR GO; GO:00069
DR GO; GO:00069
DR InterPro; IP
DR GO; GO:00069
DR FT NON TER
FT NON TER
SEQUENCE 2
RESULT 14
Q6WE65 PINMO
ID Q6WE65 PINMO I
AC Q6WE65;
DT 05-JUL-2004 (
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                                                                                                                                                                                                                                                          gene analogs from western white pine (Pindon.).";

Don.).";

Mol. Genet. Genomics 270:432-441(2004).

EMBL; AY294106; AAQ57158.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006915; P:apoptosis; IEA.

InterPro; IPR002182; NB-ARC.

Pfam; PF00931; NB-ARC; 1.
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Don.).";
Mol. Genet. (
EMBL; AY2941
GO; GO:00055
GO; GO:00069
InterPro; IP
Pfam; PF0093
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Spermatophyta
NCBI_TaxID=3:
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Pinus monticola
Eukaryota; Virid
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NON_TER
SEQUENCE
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PubMed=14586641; DOI=10.1007/800438-003-0940-1;
Liu J.-J., Ekramoddoullah A.K.M.;
"Isolation, genetic variation and expression of TIR-NBS-LRR resistance
gene analogs from western white pine (Pinus monticola Dougl. ex. D.
                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
Liu J.-J., Ekramoddoullah A.K.M.;
"Isolation, genetic variation and expression of TIR-NBS-LRR resistance
"Isolation, from western white pine (Pinus monticola Dougl. ex. D.
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ta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
3345;
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/ta; Coniferopsida; Coniferales; Pinaceae;
:3345;
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107; AAQ57159.1; -; mRNA.
524; F:ATP binding; IEA.
915; P:apoptosis; IEA.
PR002182; NB-ARC.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
S-LRR protein C603 (Fragment).
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larity 68.8%;
Conservative
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23750 MW;
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23720 MW;
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Pred. No. 11;
L; Mismatches
                                                                                                                                                                            Score 54; DB Pred. No. 11;
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Pinus; Strobus
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(TrEMBLrel.

27,

Created)

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RESULT 15
Q6HC40_BACHK
Q6HC40_BACHK
RPELIMINARY;
RPT;
Q6HC40;
Q6HC40;
Q6HC40;
DT O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DR Sacillus thuringiensis (subsp. konkukian).
OK NCBL_TRENIONAL (subsp. konkukian).
OC Bacillus thuringiensis (subsp. konkukian).
OC Bacillus cereus group.
OX NCBI_TAXID=180856;
RN (1)
RP NUCLEOTIDE SEQUENCE.
STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., O
RA Richardson P., Rubin E., Tice H.;
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., O
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; ABO17355; AAT60986.1; -; Genomic_DNA.
DR GO; GO:0015725; P:gluconate transporter activity; IEA.
DR GO; GO:0015725; P:gluconate transport; IEA.
DR InterPro; IPRO03474; Glcn_transport; IEA.
DR Gomplete proteome.
SQUENCE 250 AA; 26921 MW; 3BC16A20C586C23C CRC64;
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TOS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E Putative NBS-LRR protein GM01 (Fragment).
Name=RGA;
S Pinus monticola (Western white pine).
E Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trace Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pina
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GB: BA000004;

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RESULT 9
G71154
probable adenylosuccinate synthetase - Py:
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14
C;Accession: G71154
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organ, Reference number: A71000; MUID:9834413'
A;Accession: G71154
A;Status: preliminary; nucleic acid seque, Nolecule type: DNA
A;Residues: 1-339 <KAW>
A;Cross-references: UNIPROT:058187; UNIFA; Cross-references: UNIPROT:058187; UNIFA; Note: this accession replaces an interval.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
AIO445
probable zinc-binding dehydrogenase [impcC;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02
C;Accession: AIO445
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.
deno-Tarraga, A.M.; Chillingworth, T.; Cr
il, M.; Rutherford, K.; Simmonds, M.; Ske
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pest
A;Reference number: AB0001; MUID:21470413
A;Reference number: AB0001; MUID:21470413
A;Residues: preliminary
A;Cross-references: UNIPROT:Q8ZAW8; UNIPF
C;Genetics:
A;Gene: YPO3663
C;Superfamily: alcohol dehydrogenase; lor
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R; Takami, H.; Nakasone, K.; Takaki, Y
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of 1
A; Reference number: A83650; MUID:2051:
A; Accession: A83785
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-274 <STO>
A; Cross-references: UNIPROT:Q9KDY0; UI
A; Experimental source: strain C-125
C; Genetics:
A; Gene: fhuC
C; Superfamily: inner membrane protein
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Similarity 50.0%;
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Res. 28, 4317-4331, 2000
lete genome sequence of the alkaliphilic bacterium
nmber: A83650; MUID:20512582; PMID:11058132
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                                                                                                                                        and gene organization of the MUID:98344137; PMID:9679194
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Tanaka, T.
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Mismatches
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                                                                                                            Bequence
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Stevens,
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Davies, R.M.; D
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Yamazaki,
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PIDN: CAC93133.1

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A;Accession: E75385
A;Accession: E75385
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-311 <WHI>
A;Cross-references: UNIPROT:Q9RU69; UNIPROT:Q9RU69; Uniproces: Strain R1
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E75385
C;Species: Deinocc
C;Species: Dec-199
C;Date: 03-Dec-199
C;Accession: E7538
R;White, O.; Eiser
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A; Experimental so
C; Genetics:
A; Gene: DR1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; White, M.; Vamatheva..., M.; Shen, M.; Vamatheva..., S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. S.; Smith, H.O.; Venter, 1999
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; pMID:11418146

A;Recession: B90054
A;Recession: B90054
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <KUR>
A;Cross-references: UNIPROT:Q99RDO; UNIPARC:UPI000005488A; GB:BA000018; PID:g1370245; A;Experimental source: strain N315
C;Genetics:
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C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_rev
C; Accession: B90054
R; Kuroda, M.; Ohta, T.; Uchiyama,
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Deinococcus radiodurans
Dec-1999 #sequence_revision 03-Dec-1999 #text change na-....
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milarity 66.7%;
Conservative
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71-1577, 1999
sequence of the radioresistant bacterium Deinococcus
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Pred. No.
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                                                                Mismatches
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T.; Zalewski,
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RESULT 12

F64889

membrane protein maoC - Escherichia coli (strain K-12)

C; Species: Escherichia coli

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_chang
C; Accession: F64889

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-1;
A; Reference number: A64720; MUID: 97426617; PMID: 9278503

A; Accession: F64889

A; Status: nucleic acid sequence not shown; translation not shown; Residues: 1-681 <BLAT>
A; Cross-references: UNIPROT: P77455; UNIPARC: UPI000012EBA1; GB: A; Experimental source: strain K-12, substrain MG1655
F; 301-317/Domain: transmembrane #status predicted <TM01>
F; 588-604/Domain: transmembrane #status predicted <TM01>
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
AE2904
hypothetical protein Atu2670 [imported] -
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-
C;Accession: AE2904
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Moerage, G.; Gillet, W.; Grant, C.; Guenthn; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.;
RESULT 14
G97679
probable ATP-binding component of ABC tr
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision :
C;Accession: G97679
R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                            A; Authors: Yoo, H.; Tao, ster, E.W.
A; Title: The Genome of th A; Reference number: AB257
A; Accession: AE2904
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-264 < KUR>
A; Cross-references: UNIPF
A; Experimental source: st C; Genetics:
A; Gene: Atu2670
A; Map position: circular
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ce: strain C58 (Dupont
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Doughty,
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                                             Blanchard, ; Scott, C.;
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T.; Levy,
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T38115
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                                                                                                                                                                                                                                                   A;Reference number: Z21771
A;Accession: T38115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-255 <CON>
A;Residues: 1-255 <CON>
A;Cross-references: UNIPROT:O13888; UNIPARC:UPI000006AE18;
A;Experimental source: strain 972h-; cosmid c20G4
C;Genetics:
A;Gene: SPDB:SPAC20G4.01
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A;Accession: G97679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <KUR>
A;Cross-references: UNIPROT:Q8UC28; UNIPARC:UPI00000D1FA7; GB:AE007869; PIDN:AAK88392.1; C;Genetics:
A;Gene: AGR C_4841
A;Map positIon: circular chromosome
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C; Superfamily:
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llarity 50.0%;
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               11,
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Pred. No. 15;
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Sequence 20893, Application US/11096568A publication No. US20060048240A1 GENERAL INFORMATION: APPLICANT: Alexandrov, Nickolai et al. TITLE OF INVENTION: Sequence-Determined DNA 1 TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 20893 LENGTH: 277
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US-11-096-568A-20894
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US-11-096-568A-20893
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TITLE OF INVENTION: Sequence-Determined DNA FITTLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32256
LENGTH: 388
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NAME/KEY: misc_feature
LOCATION: (1)..(388)

OTHER INFORMATION: Ceres
3-11-096-568A-32256
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APPLICANT: Alexandrov. Nickolai
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ORGANISM: Zea mays subspreature:
NAME/KEY: misc_feature
LOCATION: (1)..(210)
OTHER INFORMATION: Ceres
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ORGANISM: Arabidopsis
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Sequence 1266, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Francisco File Reference: 2750-1592PUS2; FILE REFERENCE: 2750-1592PUS2; CURRENT APPLICATION NUMBER: US/11/096,568A; CURRENT FILING DATE: 2005-04-01; NUMBER OF SEQ ID NOS: 34471; SEQ ID NO 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA FITTLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1267
LENGTH: 246
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US-11-096-568A-1266
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                                             ; LOCATION: (1)..(28:
; OTHER INFORMATION:
US-11-096-568A-1266
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LOCATION: (1)..(277)
OTHER INFORMATION: Ceres
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NAME/KEY: misc_feature
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US20060048240A1
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Pred. No. 22;
1; Mismatches
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  Score 41.5; D
Pred. No. 26;
1; Mismatches
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PDNAV-LEGSLVKVTGANG

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TYPE: PRT

ORGANISM: Zea mays subsp;
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (316)
OTHER INFORMATION: Ceres
US-11-096-568A-1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-11-096-568A-1265
, Sequence 1265, Application US/11096568A
, Sequence 1265, Application US/11096568A
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US-11-0
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US-11-052-554A-211
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RESULT 14
US-11-096-568A-12932
; Sequence 12932, Ap
; Publication No. US
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                                                                                                                                                                                                                            TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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3-11-052-554A-211

Sequence 211, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:
                                                                                                                                                                                                               SOFTWARE: PatentIn
SEQ ID NO 211
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TITLE OF IN
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Similarity 52.6%;
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larity 57.9%;
Conservative
Application US/11096568A US20060048240A1
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GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fr

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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US-11-098-686-10580
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; LOCATION: (1)...(234)
; OTHER INFORMATION: Ceres
US-11-096-568A-12932
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US200
GENERAL INFORMATION:
APPLICANT: Kapur, Vi
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TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METI
FILE REFERENCE: 09531-128001
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TYPE: PRT
ORGANISM: Lawe
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Minimum DB Maximum DB Title: Perfect so Sequence: 3 Searched: Scoring Database protein on: processing: number score: table: 1 eq eq of. protein search, length: hits satisfying US-10-616-320A-1 98 March BLOSUM62 Gapop 10.0 , 283416 seqs, PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Minimum Match 0% Maximum Match 10 Listing first 45 **AI PDNAVLEGSLVKVTGANG** Copyright 11, 2000000000 2006, GenCore (c) 1993 using Gapext 96216763 **4** 5 100% 05:02:47 ; chosen summaries МB 0 version - 2006 residues model parameters: Search time (without ali 104.511 Mill 5.1.7 Biocceleration time 18.4127 S nt alignments) Million cell Seconds updates/sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1
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Appothetical protein Atu3180 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AP2947
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
;Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AP2947
A;Accession: AP2947
A;Status: preliminary
A;Residues: 1-277 <KUR>
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:Q8UB37; UNIPARC:UPI00000D20E7; GB:AE008689; PIDN:AAL43996.1;
A;Genetics:
A;Gene: Atu3180
A;Map position: linear chromosome RESULT 2
D98335
ABC transporter, ATP-binding protein nmb0588 [imported] - Agrobacterium tumefaciens (sti C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98335
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D98335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:Q8UB37; UNIPARC:UPI00000D20E7; GB:AE007870; PIDN:AAK90206.1; C;Genetics: AGR L 3258 멍 Ş A;Map Best Loc Matches Query e: AGR_L_3258 position: linear chromosome Local Match 25 10; 4 h 52.0%; Similarity 58.8%; 10; Conservative DNAVLEGSLVKVTGANG 20 DGAIARGSLTAVVGANG 41 Score 51; DB 2 Pred. No. 1.5; 1; Mismatches ν •• 6; Length 277; **0** Gaps 0

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RESULT 3
B83231
probable short-chain dehydrogenase PA3324 [imported] - Pseudomoc; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change
C; Accession: B83231
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warre
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.;
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAC
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Residues: 1-592 <STO>
A; Cross-references: UNIPROT:Q9HYS1; UNIPARC:UPI00000C59B4; GB:P
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA3324
                                                                                                                                                                                                pilin glycosylation protein NMA0637 [imported] - Neisseria me C;Species: Neisseria meningitidis
C;Species: 05-May-2000 #sequence_revision 05-May-2000 #text_char
C;Accession: G81983
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Chur
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, F.
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Nei
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81983
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-636 <PAR>
A;Cross-references: UNIPROT:Q9JVX3; UNIPARC:UPI00000C4A02; GE
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: pg1D; NMA0637
C;Superfamily: trsG protein
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Pred. No. 1.5;
1; Mismatches
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 [imported]
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strain Z2491
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K.R.; Kas,
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Quail,
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M.A.;
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Larbig,
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hypothetical protein Z1183 [imported] - Escherichia coli (strain O157:H7, strip) c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 c; Accession: D85608; E85659 c; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001 a; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551 a; Accession: D85608 a; Status: preliminary specimary DNA
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D8560b celiminary

substrain EDL91

D.J.; Mayhew K.; Apodaca,

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A; Reference number: AB;
A; Accession: AF2697
A; Status: preliminary
A; Molecule type: DNA
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A; Cross-references
A; Experimental sou
C; Genetics:
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                                                                                                                         A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Recession: F97479
A;Accession: F97479
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-778 <KUR>
A;Cross-references: UNIPROT:Q8UGQ3; UNIPARC:UPI00000D19D6; GB:AE007869; C;Genetics:
A;Gene: AGR C 1799
A;Map position: circular chromosome
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2697
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chereage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.;
                                                                                                                                                                                                                                                                                            R;Goodner, B.; Hi
A.; Liu, F.; Wol
Science 294, 2323
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Wollam, C.; All
2323-2328, 2001
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ALPSGSLADGTMVLLSGSNG 140
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                             DNAVLEGSLVKVTGANG 20
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Allinger,
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Pred. No.
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                                                                 Mismatches
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Lappas, C.;
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McClella
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RESULT 9
H70326
hypothetical protein aq 294 - Aquifex C; Species: Aquifex aeolicus C; Date: 08-May-1998 #sequence_revision C; Accession: H70326
R; Deckert, G.; Warren, P.V.; Gaasterle V.
Nature 392, 353-358, 1998
A; Title: The complete genome of the h; A; Reference number: A70300; MUID:98190
A; Reference number: A70300; MUID:98190
A; Residues: preliminary; nucleic acid so A; Residues: 1-371 <AQF>
A; Cross-references: UNIPROT:066644; Un A; Experimental source: strain VF5
C; Genetics: A; Gene: aq_294
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D90218
C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision
C; Accession: D90218
R; She, Q.; Singh, R.K.; Confalonieri,
Jong, I.; Jeffries, A.C.; Kozera, C.;
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricu
A; Reference number: A99139
A; Accession: D90218
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-181 < KUR>
A; Cross-references: UNIPROT: Q9UX91; U
C; Genetics:
A; Gene: rp16AB
C; Superfamily: ribosomal protein L6/L
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A;Cross-references: UNIPROT:Q8X9P2; UNIPARC:UPI00000D07CC;
A;Experimental source: strain O157:H7, substrain EDL933
A;Accession: E85659
A;Accession: E85659
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <ST2>
A;Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NIIA;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1183; Z1622
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C.; Kozera, C.J.;
A.; Sensen, C.W.;
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Medina, N.; Pe
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A; sevan, M.; Van Der Schuere
submitted to the Protein Seq
A; Reference number: Z15484
A; Accession: T06029
A; Molecule type: DNA
A; Residues: 1-532 <BEV>
A; Cross-references: UNIPROT:(
A; Experimental source: cultive
C; Genetics:
A; Gene: ATSP:T28I19.100
A; Map positi
                                                                                                                                                                                                                                                                                                                    R;Jones, K.; Graves, T.; Ozersky, P.
submitted to the EMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid W03D8.
A;Reference number: Z21249
A;Recession: T32934
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1647 <JON>
A;Residues: 1-1647 <JON>
A;Experimental source: strain Bristol N2; clone W03D8
C;Genetics:
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C;Species: Ar
C;Date: 30-Ap
C;Accession:
R;Bevan, M.;
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hypothetical protocomposition C; Species: Caenor C; Date: 29-Oct-199 C; Accession: T329 R; Jones, K.; Grav
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A; Introns: 4
1589/2
RESULT 12
A32687
Lysyl endopeptidase (EC 3.4.21.50) precursor lysyl endopeptidase (EC 3.4.21.50) precursor N; Alternate names: Achromobacter proteinase C; Species: Achromobacter lyticus C; Date: 07-Sep-1990 #sequence_revision 07-Sep C; Accession: A32687; A32960 R; Ohara, T.; Makino, K.; Shinagawa, H.; Naka
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10ces: UNIPROT:Q9T069; UNIPARC:UPI00000ABF4D;
15ces: cultivar Columbia; BAC clone T28I19
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ne EMBL Data Library, January 1998
The sequence of C. elegans cosmid W03D8.
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ilarity 52.9%;
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lopsis thaliana (mouse-ear cress)
199 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
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                                 revision 07-Sep-1990 #text_change
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J. Biol. Chem. 264, 20625-20631, 1989
A;Title: Cloning, nucleotide sequence, and expression of A;Reference number: A32687; MUID:90062204; PMID:2684982
A;Accession: A32687
A;Molecule type: DNA
A;Residues: 1-653 <OHA>
A;Residues: 1-653 <OHA>
A;Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B
R;Tsunasawa, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sak
J. Biol. Chem. 264, 3832-3839, 1989
A;Title: The primary structure and structural characteris
A;Reference number: A32960; MUID:89139439; PMID:2492988
A;Accession: A32960
A;Molecule type: protein
A;Residues: 206-473 <TSU>
A;Cross-references: UNIPARC:UPI000011061E
C;Comment: This protein specifically hydrolyzes lysyl pep
C;Keywords: hydrolase; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;201-473/Product: achromobacter proteinase I #status exp
F;211-421,217-285,241-263/Disulfide bonds: #status experification of the company of the co
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T33939
probable alcohol dehydrogenase (EC 1.1.1.
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29
C;Accession: T33939
R;Becker, M.; Graves, T.; Wilson, C.
submitted to the EMBL Data Library, Febru
A;Description: The sequence of C. elegans
A;Reference number: Z21442
A;Accession: T33939
A;Status: preliminary; translated from GB
A;Molecule type: DNA
A;Residues: 1-408 <BEC>
A;Cross-references: UNIPROT:Q9UAT1; UNIPA
A;Experimental source: strain Bristol N2;
C;Genetics:
A;Gene: CESP:D2063.1
A;Map position: 5
A;Introns: 294/3; 359/3; 373/3
C;Superfamily: alcohol dehydrogenase; lon
C;Keywords: NAD; oxidoreductase; zinc
F;47,70,173/Binding site: zinc, catalytic
RESULT 14
B46230
RNA-binding protein homolog Cpo (c
N;Alternate names: couch potato pr
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revi
C;Accession: B46230; S24678
R;Bellen, H.J.; Kooyer, S.; D'Evel
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, M.; Soejima, M.; Saki
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A;Reference number: S24677
A;Accession: S24761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-615 <BEL>
A;Cross-references: UNIPARC:UPI000017BE84; EMBL:Z14974
C;Genetics:
A;Gene: FlyBase:cpo
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A;Cross-reference extracted from NCBI backbone (NCBIN:117907,
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$24761

Cpo 61.1 protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te

C;Accession: $24761

R;Bellen, H.J.

submitted to the EMBL Data Library, August 1992
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A;Note: sequence extracted from NCBI backbone (NCBIN:117907, R;Bellen, H.J.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24677
A;Accession: S24678
A;Molecule type: DNA
A;Residues: 1-177,'T',179-311,'T',313-319,'G',321-536 <BEF>A;Cross-references: UNIPARC:UPI000017BECB; EMBL:Z14312
C;Genetics:
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A;Start codon: CTC
C;Keywords: alternative splicing; RNA binding
F;453-521/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                       A; Cross-reference
A; Start codon: CT
A; Introns: 450/1;
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A;Title: The Drosophila couch potato protein is expressed in nuclei of
A;Reference number: A46230; MUID:93051332; PMID:1427076
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Q75DJ1; Q62P10;

Q85DJ1; Q62P10;

Q75DJ1; Q62P10;

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REMBL; AE017333; AAU42873.1; -; Genomic_DNA.

REMBL; CP0000002; AAU25501.1; -; Genomic_DNA.

GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0008757; F:S-adenosylmethionine-dependent methyl InterPro; IPR002478; PUA.

R InterPro; IPR002478; PUA.

R PROSITE; PS50890; PUA; 1.

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Q9MM39;
Q1-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 1
F1 ATPase alpha subunit
                                        Mitochondrion.
Eukaryota; Viridiplantae;
Spermatophyta; Gnetophyta,
NCBI_TaxID=3383;
[1]
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Gnetum ula.
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MEDLINE=20226063; PubMed=10760278;
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DE ATPase alpha s
GN Name=atp1;
OS Gnetum gnemon
OG Mitochondrion.
OC Eukaryota; Vir
OC Spermatophyta;
OX NCBI TaxID=338
RN [1]
RP NUCLEOTIDE SEC
RX MEDLINE=200521
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RA Qiu Y.L., Lee
RA Qiu Y.L., Lee
RA Zanis M., Zimn
RT nuclear genome
RI Nature 402:404
CC -i- SIMILARITY
DR EMBL; AF19761;
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DR GO; GO:004526;
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X MEDLINE=20052162; PubMed=10586879; DOI=10.1038/46536;
X MEDLINE=20052162; PubMed=10586879; DOI=10.1038/46536; C. Savolainen V., Chase M.W.;
X A Coin W.L., Lee J., Savolainen V., Chase M.W.;
X Nature 402:404-407(1999).
X Nature 402:404-407(199).
X Nature 402:404-407(1999).
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SMR; Q9MM39; 1-399.

GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:00045261; C:proton-transporting ATP synthase complex, C. . . .

GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.

GO; GO:0016469; C:proton-transporting ATP synthase activity. . . .

GO; GO:0016469; F:hydrogen-transporting ATP synthase activity, rota. . .

GO; GO:0046933; F:hydrogen-transporting ATPase activity, rota. . .

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .

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TY: Belongs to the ATPase alpha/beta chains family.
09; AAF64667.1; -; Genomic_DNA.
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seed plants based on all three genomic compartments:
sperms are monophyletic and Gnetales' closest relative
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R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016820; F:hydrolase activity; IEA.
R GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid.
R GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
R GO; GO:0015992; P:proton transport; IEA.
R GO; GO:0015992; P:proton transport; IEA.
InterPro; IPR0005294; ATP_synthfl_alph.
InterPro; IPR000793; ATPase_a/b_C.
R InterPro; IPR000194; ATPase_a/b_N.
R InterPro; IPR000194; ATPase_a/b_Centre.
R Pfam; PF00006; ATP-synt_ab; 1.
R Pfam; PF00306; ATP-synt_ab; 1.
R Pfam; PF00306; ATP-synt_ab_N; 1.
R Pfam; PF02874; ATP-synt_ab_N; 1.
R Pfam; PF00306; ATP-synt_ab_N; 1.
R PF003152; ATPASE_ALPHA_BETA; 1.
R PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
R PROSITER 418 418
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RESULT 9
Q6BIS4_DEBHA
ID Q6BIS4;
AC Q6BIS4;
DT 25-OCT-2004 (TrEMBLrel. 28, Last 0)
DT 25-OCT-2004 (TrEMBLrel. 28, Last 0)
DT 25-OCT-2004 (TrEMBLrel. 28, Last 0)
DE Similar to CA1657 | IPF16022 Candidon
DE function.
GN OrderedLocusNames=DEHA0G086799;
OS Debaryomyces hansenii (Yeast) (To100)
CC Eukaryota; Fungi; Ascomycota; Saconcharomycetales; Saccharomycetales; Saccharomy
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RA Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
"The early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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(Fragment).
ORFNames=GSTENG00029526001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC | STRAIN=ATCC 36239 / CBS 767; PubMed=15229592; DOI=10.1038/nature02579; Dujon B., Sherman D., Fischer G., Durrens
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
cetales; Saccharomycetaceae; Debaryomyces.
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., de Montigny J., Marck C., Neuveglise C., Talla E.,
Frangeul L., Aigle M., Anthouard V., Babour A., Barbe
llanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
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A1657|IPF16022 Candida albicans IPF16022 unknown
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QBG456_BIFLO
QBG456;

AC QBG456;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence upd
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation u
DE Fas.

GN Name=fas; OrderedLocusNames=BL1537;

DS Bifidobacterium longum.

CC Bacteria; Actinobacteria; Actinobacteridae; B
DC Bifidobacteriaceae; Bifidobacterium.

NCBI_TaxID=216816;
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Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth
Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenb
Wincker P., Souciet J.-L.;
"Genome evolution in yeasts.";
Nature 430:35-44(2004).
REMBL, CR382139; CAG90360.1; -; Genomic_DNA.
RINterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 6.
SMART; SM00320; WD40; 6.
SMART; SM00320; WD40; 6.
Complete proteome; Repeat; WD repeat.

SEQUENCE 1048 AA; 117153 MW; 7BAEB602ACF85373 CRC64;
to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2(
REMBL; AE014295; AAN25329.1; -; Genomic_DNA.
RGO; GO:0005835; C:fatty acid synthase complex;
GO; GO:0016491; F:fatty-acid synthase activity;
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:00066118; P:electron transport; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
InterPro; IPR00136; 2nprop_dioxygen.
InterPro; IPR001227; Ac_transferase.
InterPro; IPR003965; Fatty_acid_synth.
InterPro; IPR003965; Fatty_acid_synth.
InterPro; IPR003965; Fatty_acid_synth.
InterPro; IPR002539; MaoC_dehydratas.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
Pfam; PF03060; NPD; 1.
PRINTS; PR01483; FASYNTHASE.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_
Complete proteome.
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MEDLINE=22294977; PubMed=12
Schell M.A., Karmirantzou M
Pessi G., Zwahlen M.-C., De
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pessi G., Zwamie..
Pridmore R.D., Arigoni F.;
Pridmore R.D., Arigoni F.;
Pridmore R.D., Arigoni F.;
"The genome sequence of Bifidobacterium longuither to the human gastrointestinal tract.";
to the human gastrointestinal tract.";
Natl. Acad. Sci. U.S.A. 99:14422-14427
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B., Vilanova D., Berger
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ATCC 15692 / PAO1;

ATCC 15692 / PAO1;

20437337; PubMed=10984043; DOI=10.1038/35023079;

C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;

te genome sequence of Pseudomonas aeruginosa PAO1, an

nistic pathogen.";

406:959-964(2000).

E004754; AAG06712.1; -; Genomic_DNA.
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STRAIN-B728a;

DOE Joint Genome Institute;

A Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Tr

A Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Dette

A Nolan M., Richardson P.M., Kyrpides N.C., Ivanova N.;

"Comparison of two complete genome sequences of Pseudomonas syr

pv. syringae B728a and pv. tomato DC3000.";

Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
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STRAIN=B728a;
Feil H., Feil W.S., Lindow S.E.;
Feil H., Feil W.S., Lindow S.E.;
Submitted (MAY-2005) to the EMBL/GenBan Submitted (MAY-2005) to the EMBL/GenBan EMBL; CP000075; AAY37077.1; -; Genomic InterPro; IPR005546; Auto_transporter.

InterPro; IPR006315; Autotransporter.
InterPro; IPR004899; Pertactin_C.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01484; PRTACTNFAMLY.
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SEQUENCE 732 AA; 75763 MW; 4C355FC1
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Name=lig; OrderedLocusNames=PF1635; Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Pyrococcus.

NCBI_TaxID=2261; [1]
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Pseudomonas syringae pv. syringae pv.
                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE (STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8. Mathur E.J., Marsh E.J., Schoettlin W.E.; "Purified thermostable Pyrococcus furiosus Patent number US5700672, 23-DEC-1997.
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Robb F.T., Brown J.R.;

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.1; -; Genomic_DNA.
o_transptbeta.
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Gammaproteobacteria;
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Pred. No. 1.2e
1; Mismatches
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on update)
(Polydeoxyribonucleotide
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1.2e+02;
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, Detter J.
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RESULT 14
Q6AHE3 LEI
ID Q6AHE
AC Q6AHE
AC Q6AHE
DT 25-OC
DT 25-OC
DT 25-OC
DT 25-OC
CO Name=
OS Leife
OC Micro
OC Micro
OX NCBI
RN [1]
RY NUCLI
RC STRAI
RX PUDMORT
RA MONTO
RA Kita;
RA Monto
RA Takit
RA Alme:
RA Goldt
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R InterPro; IPR012309; DNA ligase A C.

R InterPro; IPR012310; DNA ligase A M.

R InterPro; IPR012310; DNA ligase A M.

R InterPro; IPR012340; OB NA bd sub.

R InterPro; IPR012340; OB NA bd sub.

R PANTHER; PTHR10459; DNA ligase; 1.

Pfam; PF04679; DNA ligase A M; 1.

R Pfam; PF04675; DNA ligase A M; 1.

R Pfam; PF04675; DNA Ligase A N; 1.

R Pfam; PF04675; DNA LIGASE A1; 1.

R PROSITE; PS00697; DNA LIGASE A1; 1.

R PROSITE; PS00333; DNA LIGASE A2; FALSE NEG.

R PROSITE; PS50160; DNA LIGASE A3; 1.

R PROSITE; PS50160; DNA LIGASE A1; 1.

R PROSITE PROSITE A1; 1.

R PROSITE PRO
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Matche
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Q6AHE3_LEIXX
Q6AHE3;
Q6AHE3;
25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
Alcohol dehyd
Name=adhT; Or
Leifsonia xyl
Bacteria; Act
Micrococcinea
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                                                                 Monteiro-Vitc
Kitajima J.P.
de Oliveira J
Takita M.A.,
                                                                                                                                                        NUCLEOTIDE SE
STRAIN=CTCBO
PubMed=153056
                     Takita N
Almeida
Ferro M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 100 degrees Celsius. Thermostable;
SUBUNIT: Monomer.
SIMILARITY: Belongs to the ATP-dependent DNA ligase family.
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                                                                                                                                                                                                                                                                                                                                                                drogenase.
 Corello C.B., Camargo L.E.A., Van Sluys M.A.,
P., Truffi D., do Amaral A.M., Harakava R.,
J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
da Silva A.C.R., Furlan L.R., Carraro D.M., Ca
Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,
, Gagliardi P.R., Giglioti E., Goldman M.H.S.,
, Kimura E.T., Ferro E.S., Kuramae E.E., Lemos
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tinobacteria; Actinobacteridae; A
ae; Microbacteriaceae; Leifsonia.
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                                                                                                                                                                                                        EQUENCE.
                                                                                                                                                                                                                                                    9736;
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                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.1e+02
4; Mismatches
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534158525B9D24B2
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17

Job

time

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122.0

95 весв

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RESULT 15

Q97AQ8_THEVO PRELIMINARY; PRT; 404 AA.

AC Q97AQ8;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 26, Last annotation update)

DT 01-OCT-2004 (TrEMBLrel. 26, Last annotation update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Carboxypeptidase.

QN carchaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

CARCHITEMBLRE SEQUENCE (LARGE SCALE GENOMIC DNA).

RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).

RR MEDINDR-20570466; PubMedail121011; DOI=10.1073/pnas.97.26.1425

RX MEDLINB-20570466; PubMedail121011; DOI=10.1073/pnas.97.26.1425

RX MEDLINB-20570466; PubMedail121011; DOI=10.1073/pnas.97.26.1425

RX MEDLINB-20570466; PubMedail121011; DOI=10.1073/pnas.97.26.1425

RX Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Kawa Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanehbori K., Suzuki M., Kawashima-Ohya Y., Matanabe Activity; IEA.

DR GO; GO:000633; F:metailopeptidase M20.

DR TICRPAMS; TIRROLISS; M20 dimer; 1.

DR TIRROLISS; M20 dimer; 1.

DR GO; GO:0006468; Augustion K., Suzuk
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HA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Nunce L.R., Oliveira R.C., Siqueira W., de Souza A.A.,

HA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

HA Nunce L.R., Oliveira R.J., Siqueira W., de Souza A.A.,

HA Nunce L.R., Oliveira R.J., Siqueira W., de Souza A.A.,

HA Nunce L.R., Oliveira R.J., Siqueira W., de Souza A.A.,

HA Nunce L.R., Oliveira R.J., Siqueira W., de Souza A.A.,

HA Nunce L.R., Oliveira R.J., Siqueira G.G., Siqueira W., de Souza A.A.,

HA Nunce L.R., Oliveira R.J., Siqueira R.J., Siqueira R.J.,

HA Nunce L.R., Oliveira R.J., Siqueira R.J., Siqueira R.J., Siqueira R.J.,

HA Nunce L.R., Oliveira R.J., Siqueira R.J., Siqueir
                                                                                                                                                                                                                                                                                   P NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

C STRAIN=GSS1 / DSM 4299 / JCM 9571;

X MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;

A Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

A Kawashima T., Yamamoto Y., Aramaki M., Kanehori K., Kawamoto T.

A Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

EMBL; BA000011; BAB59893.1; -; Genomic_DNA.

MEROPS; M20.008; -.

R GO; GO:0004180; F:carboxypeptidase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0006237; F:metallopeptidase activity; IEA.

GO; GO:0006508; F:proteolysis and peptidolysis; IEA.

InterPro; IPR011650; M20_dimer.

IN InterPro; IPR011650; M20_dimer.

IN Pfam; PF01546; Peptidase M20_ amidh.

Pfam; PF01546; Peptidase M20_ amidh.

Pfam; PF01546; Peptidase M20; 1.

TIGRFAMs; TIGR01891; amidohydrolases; 1.

Carboxypeptidase; Complete proteome.

Carboxypeptidase; Complete proteome.
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Similarity 60.0%;
12; Conservative
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                                                                                                                                                  49.0%;
Similarity 81.8%;
9; Conservative
IPDNAVLEGSL
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    271
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                                                                                                                                                  Score 48; DB Pred. No. 94; 2; Mismatches
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ed. No. 79;
Mismatches
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                                               (R)-hydroxy ester; aldehyde reductase
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                                                                                                                                                                                                                invention relates to a method of preparing high yields of an (R) roxy ester by reducing an alpha-keto ester using a ketoreductase yme. The present sequence represents Sporobolomyces salmonicolor oreductase, aldehyde reductase II used in the method of the inver
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j ketoreductase enzyme and non-ketoreductase (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ion relates to a method of preparing high yields of an (R)-ter by reducing an alpha-keto ester using a ketoreductase e present sequence represents a Sporobolomyces salmonicolor ase, aldehyde reductase II, N-terminal peptide used in the
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                                                               431257/40.
                                   (R)-hydroxy ester involves adding alpha-keto ester ketoreductase enzyme and non-ketoreductase enzyme
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ilarity 81.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         he invention.
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                                                                                Sturr MG,
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                                                                                                                                                                                                                                                                ces salmonicolor aldehyde reductase
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                   NO 1;
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promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant having an improved property comprises transforming a transformed plant having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nyaroxy ester by reducing an alpha-keto ester using a ket enzyme. The present sequence represents a Sporobolomyces ketoreductase, aldehyde reductase II, N-terminal peptide method of the invention.
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                                                                                                                                                                                                         Claim
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(HINK/)
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imilarity 88.9%;
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                         iion relates to an isolated nucleic acid molecule. The methods sitions of the present invention are useful for diagnosing sating Neisserial bacterial infections, in particular meningitis semia caused by Neisseria meningitidis and Neisseria gonorrhea. It sequence represents the amino acid sequence of a N. It septence of a N. It septence in the sequence data for this patent did not form the printed specification, but was obtained in electronic formatic printed specification.
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RESULT 12
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DE N. gonorr
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PN W02002792
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        Disclosure;
                          New protein medicament
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N-PSDB; ABZ38178.
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P-PSDB;
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                                                               sequences AAY38499-Y38944 represent Neisseria meningitidis and sae antigenic proteins. They are encoded by open reading ) AAZ11972-Z12358. The antigenic proteins, their fragments, cacids and antibodies are used for diagnosis, prevention (as treatment of Neisseria infections, such as meningitis, and gonorrhea. Both organisms are closely related. Fragments sic acids are useful as hybridisation probes and antisense
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Mismatches
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diagnosis,
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                                                                                                                                                        on relates to an isolated nucleic acid molecule. The methods tions of the present invention are useful for diagnosing ting Neisserial bacterial infections, in particular meningitis mia caused by Neisseria meningitidis and Neisseria gonorrhea. sequence represents the amino acid sequence of a N. s protein. Note: The sequence data for this patent did not the printed specification, but was obtained in electronic ctly from USPTO at
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RESULT 9
US-09-543-681A-6546
• Sequence 6546, App
Sequence 6546, Application US/09543681A; Patent No. 6605709; GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITILE OF INVENTION: DIAGNOSTICS AND THERAPEUSICE REFERENCE: 2709.1002-001; CURRENT APPLICATION NUMBER: US/09/543,681A; CURRENT FILING DATE: 2000-04-05; PRIOR APPLICATION NUMBER: US 60/128,706; PRIOR FILING DATE: 1999-04-09; NUMBER OF SEQ ID NOS: 8344; SEQ ID NO 6546
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US-09-489-039A-13937
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LENGTH: 340
TYPE: PRT
ORGANISM: Corynahas
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CURRENT APPLICATION NUMBER: US/09/605,70
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
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LENGTH: 687
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES
TITLE OF INVENTION: PROTEINS
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09-489-039A-13937
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Similarity 38.1%;
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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ORGANISM: PB
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TITLE OF INVENTION:
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SEE: Medlen & Carroll, LLP
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San Francisco
California
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Weinfeld, Michael
INFORMATION:
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BER: US 60/074,788
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US-09-650-855-101
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TITLE OF INVENTION: DETECTION AND QUANT:
TITLE OF INVENTION: POLYMORPHISMS, DNA I
TITLE OF INVENTION: DNA DAMAGE AND DNA I
FILE REFERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651,650
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
                    APPLICANT: LAWRENCE LIVERMOR TITLE OF INVENTION: CHIMERIC TITLE OF INVENTION: MUTATION TITLE OF INVENTION: MISMATCH FILE REFERENCE: IL-10284 CURRENT APPLICATION NUMBER: UCURRENT FILING DATE: 2000-08 PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 2000-03-2
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GENERAL INFORMATION:
APPLICANT: MCCUTHE
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Patent No. 634050
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09-651-656-101
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TYPE: PRT
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 940 amino acide
           NUMBER OF
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REGISTRATION NUMBER: 32,8
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 705-8410
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TOPOLOGY: unl
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PatentIn
                                                                                       MCCUTHEN-MALONEY, SANDRA
LAWRENCE LIVERMORE NATIONAL LABORATORY
VENTION: CHIMERIC PROTEINS FOR DETECTION AND
VENTION: MUTATIONS, DNA SEQUENCE VARIATIONS,
VENTION: MISMATCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCCUTHEN-MALONEY, SANDRA
LAWRENCE LIVERMORE NATIONAL LABORATORY
JENTION: DETECTION AND QUANTITATION OF
JENTION: POLYMORPHISMS, DNA SEQUENCE VI
JENTION: DNA DAMAGE AND DNA MISMATCHES
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2000-08-29
BER: 60/192,764
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC:
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOI
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3792
LENGTH: 111
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US-09-134-000C-37
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
EQ ID NO 8607
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ORGANISM:
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Search completed: March 11, Job time : 31.0317 secs

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GENERAL INFORMATION:
APPLICANT: Jefferey C. Moore
APPLICANT: Michael G. Sturr
APPLICANT: Kathleen McLaughlin
APPLICANT: Jaehon Kim
TITLE OF INVENTION: PROCESS FOR REDUCING AN FILE REFERENCE: 21115
CURRENT APPLICATION NUMBER: US/10/616,320A
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-616-320A-4
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US-10-616-320A-1
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                                                  RESULT 9
US-10-369-493-14080
; Sequence 14080, Application US/
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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Publication No. US20040101937A1
GENERAL INFORMATION:
APPLICANT: Jefferey C. Moore
APPLICANT: Michael G. Sturr
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LENGTH: 20
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Similarity 81.8%;
18; Conservative
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6; Conservative
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                                      Cao,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kathleen Mc
Jaehon Kim
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Cao, Yongwei
Hinkle, Gregory
Slater, Steven C
Goldman, Barry S
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Pred. No. 0.
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APPLICANT:

SENOH, ANALISENOH, MASATO

APPLICANT

INVENTION:

NOVEL POLYNUCLEOTIDES

APPLICANT:

ANDO, SEINC HAYASHI, MIKIRO OCHIAI, KEIKO YOKOI, HARUHIKO TATEISHI, NAOKO SENOH, AKIHIRO

APPLICANT:

WALL
NAKAGAWA, S.
NIZOGUCHI, H.
NIDO, SEIKO
NIDO, MIK

SATOSHI HIROSHI

APPLICANT: APPLICANT:

APPLICANT:

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JS20030233675A1

JS20030233675A1

LANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20309

LENGTH: 339

TYPE: PRT

ORGANISM: PV-

US-10-369-4^*
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ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITITLE OF INVENTION: US 40/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14080
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                                                    RESULT 11
US-09-738-626-6285
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Best Local S
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Publication No. US20020197605A1
GENERAL INFORMATION:
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milarity 59.1%;
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larity 64.7%;
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REFERENCE:

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RESULT
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6285
LENGTH: 340
TYPE: PRT
                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of ExFILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,12
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
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                                         PRIOR FILI
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NUMBER OF
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APPLICANT:
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                            SOFTWARE:
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LENGTH:
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                                                                                                             R FILING DATE: 2000-09-06
R APPLICATION NUMBER: 60/230,347
R FILING DATE: 2000-09-09
R APPLICATION NUMBER: 60/242,578
R FILING DATE: 2000-10-23
R APPLICATION NUMBER: 60/253,625
R APPLICATION NUMBER: 60/253,625
R APPLICATION NUMBER: 60/257,931
R APPLICATION NUMBER: 60/267,636
R APPLICATION NUMBER: 60/267,636
                                                                                   APPLICATION NUMBER:
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                                                                                                     FILING DATE:
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67877, Apr
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                           PatentIn
                                                      Prior Application data
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Carr, Grar
Yamamoto,
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Wall, Dar
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Malone, Cheryl
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Ohlsen, Kari
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dio, Carlos
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RESULT 14
US-10-450-763-39265
; Sequence 39265, Application No. US2000; Publication No. US2000; GENERAL INFORMATION:
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US-10-662
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US-10-662-358-
                                                                                                                                                                                                    FILE OF INVENIOUS
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-10-662-358-1
Sequence 1, Application Sequence 1, Application Publication No. US200 GENERAL INFORMATION:
APPLICANT: LEE, Sang APPLICANT: PARK, Siritle OF INVENTION:
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                                                                                                                                                                                          NUMBER OF SOFTWARE:
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PRIOR FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Pataner
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2003-
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hys
NAME/KEY: DOMAIN
LOCATION: (940)..(982)
LOCATION: 1940)..(982)
OTHER INFORMATION: Aldehyde dehydrogenases glutamic acid proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00687B, p-value of 17.54
OTHER INFORMATION: 22, raw score of 17.54
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nilarity 36.4%;
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illarity 36.8%;
Conservative
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US20050196754A1
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K, Si Jae
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 48; DB 5;
ed. No. 1.1e+02;
Mismatches 4
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WS-10-369-493-11253

US-10-369-493-11253

Sequence 11253, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11253
LENGTH: 276
TYPE: PRT
ORGANISM: Methanosarcina mazei
US-10-369-493-11253
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Search completed: March Job time: 102.968 secs
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Best Local S
Matches 7
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Best Local Similarity 55.6%;
Matches 10; Conservative
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993 VDSGLVPEGAISLICGSAG 1011
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112 NSAVEMEGSKIVVTGAGG
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7; Conservative 8
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                                                                                                                          Score 47; DB 4;
Pred. No. 57;
4; Mismatches
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; TYPE: PRT
; ORGANISM: Pseu
US-11-087-099-9804
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US-11-087-099-9804
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US-11-082-389-168
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                              ; TYPE: PRT
; ORGANISM: Corynebacterium
US-11-082-389-168
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
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Best Local S
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NUMBER OF SEQ
SEQ ID NO 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes and Uses for Plant FILE REFERENCE: 38-21(53450)B EP CURRENT APPLICATION NUMBER: US/11/087,099 CURRENT FILING DATE: 2005-03-22 NUMBER OF SEQ ID NOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US2
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS !
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
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Match
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                                                                                                                                                        FILING DATE: 1999-08-31
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8; Conservative
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Zelder, Oskar
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o. US20050244935A1
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US20060041961A1
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41.18;
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Pred. No. 7.5;
4; Mismatches
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APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 162
LENGTH: 363
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US-10-873-9
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                                                                                                                                          ; TYPE: PRT; ORGANISM: Clostridium acetobutylicum US-11-087-099-766
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US-11-087-0
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APPLICANT: Microbial
RESULT
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                                                                                                                                                                                   SEQ ID NO 766
LENGTH: 455
                                                                                                                Query Match
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10-873-528-1
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Similarity 50.0%;
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NITIPKGSLFTLLGASG
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5. US20050276814A1
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                                      VILNYIMPEGVFVLIT
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. US20060041961A1
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Conservative
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                                                                                        Score 44; DB Pred. No. 25; 4; Mismatches
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US-10-793-626-284; Sequence 284, A; Publication No.

Application US/10793626 . US20050255478A1

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Sequence 4407, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA; TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2; CURRENT APPLICATION NUMBER: US/11/096,568A; CURRENT FILING DATE: 2005-04-01; NUMBER OF SEQ ID NOS: 34471; SEQ ID NO 4407
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA FITTLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4406
LENGTH: 228
                                                                                                                  RESULT 13
US-11-096-568A-4406
; Sequence 4406, Application US/1; Publication No. US20060048240A1
; GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; LOCATION: (1)..(211)
; OTHER INFORMATION: Cert
US-11-096-568A-4407
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-793-626-284
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US-11-096-568A-4407
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APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMII
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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Best Local S
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Similarity 47.1%;
8; Conservative
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Similarity 31.8%;
7; Conservative
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APPLICANT: MUN...

APPLICANT: MUN...

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10,

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 3300

TNGTH: 241

Teria gonorrhoeae
                                                                                                     Sequence 12277, Application US/11087099; Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Im
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 12277
LENGTH: 336
TYPE: PRT
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Best Local S
Matches
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(228)
OTHER INFORMATION: Ceres Seq. I
S-11-096-568A-4406
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Best Local
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                                               Query Match
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PIZZA Mariagrazia
MASIGNANI Vega
MONACI Elisabetta
VVENTION: GONOCOCCAL PROTEINS AND
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US20050260581A1
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                                    Score 43; DB Pred. No. 24; 2; Mismatches
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Search completed: March 11, 2006, 05:16:52 Job time : 11.873 secs 159 AKVKEGQRVLITGAGG 174

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